

FIG. 1A

MAJORITY	ATGXXGGCGATGCTTCCCCCTCTTTGAGCCCAAGGCCGGGTCTCTCTGGTGACGGGCACCTTGGCCT	
DNAPTAQ	...AG..G.....G.....G.....	70
DNAPTFLC..G.....	67
DNAPTTH	...GA.....G.....A.....	70
MAJORITY	ACCGCACCTTCTTCGCCCTGAAGGGCCTCACCACCACCGGGGGAACCGGTGCAGGGGTCTACGGCTT	
DNAPTAQCA.....G..G.....	140
DNAPTFLT.....C.....C..T.....	137
DNAPTTHG.....	140
MAJORITY	CGCCAAGAGCCTCCTCAAGGCCCTGAAGGAGGACGGGGACXXGCCGGTGTCTTGTGACGCCAAG	
DNAPTAQC.....A.....	207
DNAPTFLA.....GT..T.....	204
DNAPTTHT..AA..C..CT.....	280
MAJORITY	GCCCCCTCCTTCGCGCCACGAGGCCTACGAGGCCTACAAGCGGGCGGCCACCCCGGAGGACTTTC	
DNAPTAQG..GG.....G.....	277
DNAPTFLGA.....G.....C.....	274
DNAPTTHG.....C.....	280
MAJORITY	CCCGGCAGCTCGCCCTCATCAAGGAGCTGGTGGACCTCCTGGGGCTTGGCGCCTCGAGGTCCCCGGCTA	
DNAPTAQA.....G.....G.....	347
DNAPTFLG.....T.....A..C.....T..G..G.....T.....	344
DNAPTTHT.....T..A.C.....	350

FIG. 2A

MAJORITY	CGAGGCGGACGACGT	CTGGCCACCCCTGGCC	AAGGCGGAAAGGAGGGGTACGAGGTGCGCATCCTC
DNAPTAQC.....G.....C.....	417
DNAPTFL	T.....G.....CG.....	414
DNAPTTHT..C.....	420
MAJORITY	ACGCGCGACCGGACCTCTAC	CAGCTCCTTTCCGACCGCATCGCCGTCTCCACCCCGAGGGGTACCTCA	
DNAPTAQAAA.....T.....CA.....	487
DNAPTFL	..T.....G..G.....A.....T.....	484
DNAPTTHA..G.C.....G.....	490
MAJORITY	TCACCCCGCGGTGGCTTTGGGAGAAAGTACGGCCTGAGGCCGGAGCAGTGGGTGGACTACCGGGCCCTGGC		
DNAPTAQC.....A.....C..C.....CC.....	557
DNAPTFLAC.....C.C.....	554
DNAPTTHA.....C.....T..C.....C.T	560
MAJORITY	GGGGACCCCTCCGACAACTCTCCCGGGGTCAAGGGCATCGGGGAGAGACCGCCCGAAGCTCCTCXAG		
DNAPTAQ	C.....GAG.....T.....G..GAG.....	627
DNAPTFLG..T..A.....G.....A..G.....A..CGC	624
DNAPTTHTC.....A..	630
MAJORITY	GAGTGGGGAGCCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAAGCCCGC	...CXTCCGGGAGAAGA	
DNAPTAQGC.....C.....A.....	694
DNAPTFLT..C..C.....A.....T..G.....	691
DNAPTTHA.....A..A.AAA.G.....	700

FIG. 2B

MAJORITY	TCCAGGGCCACATGGAXGACCTGAXGCTCTCCTGGGAGCTXTCCAGGTGCGCACCGACCTGCCCCCTGGA	
DNAPTAQ	...T.....C..T...A.....C..GG..A.....	764
DNAPTFL	...GGG...G.C...GCC..T...C..A...T...A...T...	761
DNAPTTH	...A.....C.....A.....C.G...T.....C.....G.....C.....	770
MAJORITY	GGTGGACTTCGCCAAGXGGCGGGGAGCCCGACCGGAGGGGCTTAGGGCCTTTCTGGAGAGGCTGGAGTTT	
DNAPTAQAA.....A.....A.....T.....T.....T.....	834
DNAPTFLGG.G.C.C..CACA...A...T.....T..GC...T...T...C..T.....	831
DNAPTTHC.....C.G.....C.....C.....C.....C.....C.....	840
MAJORITY	GGCAGCCTCCTCCACGAGTTCGGCCTTCCTGGAGGGCCCCAAGGCCCTGGAGGAGGCCCTGGCCCCCGC	
DNAPTAQT.....T.....AA.....	904
DNAPTFL	...A.....G.....G.....G.....G.....G.....G.....G.....G.....T...	901
DNAPTTHC.....C.....GCCC.....	910
MAJORITY	CGGAAGGGCCTTCGTGGGCTTTGTCCCTTTCCCGCCCCCGAGCCCATGTGGGCCGAGCTTCTGGCCCTGGC	
DNAPTAQG.....AAG.....T.....	974
DNAPTFL	...T..TT.....TC.T.....T.....	971
DNAPTTHC.....C.....G.....AAA.....	980
MAJORITY	CGCCGCCAGGGGCGGGTCCACCGGGCACCAGACCCCTTTAXGGGCCTXAGGGACCTXAAGGAGGTG	
DNAPTAQG.....C..C..G..T.A..AA.C..C.....G.....C...	1044
DNAPTFL	T.GG..GT.....G..CC...T.....A.....C.....G.....T.....G.....	1041
DNAPTTH	...TG.....C.....G.....G.....GGC...G..A..A.....C.....C.....C.....	1050

FIG. 2C

MAJORITY	CGGGGXCTCCTCGCCCAAGGACCTGGCCGTTTTTGGCCCTGAGGGAGGGCCTXGACCTCXTGCCCCGGGGACG	
DNAPTAQG..T.....A.....AG.....C.....A.....T.G.....CC.....C.....	1114
DNAPTFLAA.....G.....G.....C.....C.....T.C..A.A.....	1111
DNAPTTHC.....C.....C.....TC.....G..A.....G.....	1120
MAJORITY	ACCCCATGCTCCTCGCCTACCTCCTGGACCCCTCCAACACCACCCCGAGGGGTGGCCCCGGCGCTACGG	
DNAPTAQT.....	1184
DNAPTFLG.....T.....T.....T.....	1181
DNAPTTHG.....G.....	1190
MAJORITY	GGGGGAGTGGACGGAGGAXGCGGGGAGCGGGCCCTCCTXTCCGAGAGGCTCTTCCXGAACCTXXXGGAG	
DNAPTAQ	C.....G.....G.....GC.....T.....GCC.....GTG..G.	1254
DNAPTFLT.....A.....GG.....C.C.....A..C...AAA.....	1260
DNAPTTHC..C.CCC.C.....C..G.....CAT.G.....CCTTA..	1260
MAJORITY	CGCCTTGAGGGGAGGAGGGCTCCTTTGGCTTTACCAGGAGGTGGAGAAGCCCTTTCCCGGGTCCIGG	
DNAPTAQ	A.G.....G.....G.....G.....GCT.....	1324
DNAPTFLA...A..A..AC.C..G.....G.....G.....GT...	1321
DNAPTTHC.....A.....C.....C.....A.....C.....	1330
MAJORITY	CCCACATGGAGGCCACGGGGGTXCGGCTGGACGTGGCCTACCTCCAGGCCCTXTCCCTGGAGGTGGCGGA	
DNAPTAQG..C.....T...AG.....T.G.....C...	1394
DNAPTFL	..GG.....C.....C.....C.....A..C	1391
DNAPTTHC.....A.....T.....T.....C.T.....	1400

FIG.2D

MAJORITY	GGAGATCCGCCCTCGAGGAGGAGGTCTTCCGCCTGGCCGGCCACCCCTTCAACCTCAACTCCCCGGGAC	
DNAPTAQGC.....CC.....	1464
DNAPTFLG.G.....AG..G.....C.....	1461
DNAPTTHT.....T.....G.....	1470
MAJORITY	CAGCTGGAAGGGTGCTCTTTGACGAGCTXGGGCTTCCCGCCATCGGCAAGACGGAGAAGACXGGCAAGC	
DNAPTAQC.....A.....C.....	1534
DNAPTFLGC.....G.C..G..T.....G..G..A..	1531
DNAPTTHTA.....T.G..G.....C.A.....A.....	1540
MAJORITY	GCTCCACCAGCGCCCGTGCTGGAGGCCCTXCGXGAGGCCACCCCATCTGTGGAGAAGATCCTGCAGTA	
DNAPTAQC.....C..C.....	1604
DNAPTFLT.....G..A.....CCGC.....	1601
DNAPTTHG.....A..G.....C...C..	1610
MAJORITY	CCGGGAGCTCACCAAGCTCAAGAACACCTACATXGACCCCTGCGCXGXCCTCGTCCACCCAGGACGGGC	
DNAPTAQG...G.....T.....T...G.A...A.....	1674
DNAPTFLA.....A.....C.C..G.....A..C...	1671
DNAPTTHG.G.....AAG.....G.....	1680
MAJORITY	CGCCTCCACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTTAGTAGCTCCGACCCCAACCTGC	
DNAPTAQA.....A.....T.....C..	1744
DNAPTFLG.....C.....TCC.....	1741
DNAPTTHG.....G.....	1750

FIG. 2E

MAJORITY	AGAAATCCCCCGTCGACACCCXCTGGGCCAGAGGATCCGCCGGGCTTCGTGGCCGAGGAGGGXTGGGT	
DNAPTAQG..T..G.....A.C.....G...C.	1814
DNAPTFLG.....T.....C.C.....A.....C.....	1811
DNAPTTHCT.....C.....T.....C	1820
MAJORITY	GTTGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCTCGGCCACCTCTCCGGGGACGAGAACCTG	
DNAPTAQ	A.....A.....G.....C.....	1884
DNAPTFL	.C.....T.T.....C.....T.....	1881
DNAPTTHC.....C.....A.....	1890
MAJORITY	ATCCGGGTCTTCCAGGAGGGGAGGACATCCACCCAGACCCGACGCTGGATGTTCCGGCGTCCCCCCCGG	
DNAPTAQC.....GG.....G..	1954
DNAPTFLT.....A.....TT.....C.	1951
DNAPTTH	...A.....A.....A.....	1960
MAJORITY	AGGCCGTGGACCCCTGATGCGCCGGCGGCCAAGACCATCAACTTCGGGGTCTCTACGGCATGTCCGC	
DNAPTAQG..	2024
DNAPTFL	.A.GG..A.....T.....G.....	2021
DNAPTTHGG.G.....C.....	2030
MAJORITY	CCACCGCCTCTCCAGGAGCTTGCCCATCCCCCTACGAGGAGGGGTGGCCCTTCATTGAGCGCTACTTCCAG	
DNAPTAQA.....T.....CCA.....T...	2094
DNAPTFLGG.....T.....	2091
DNAPTTH	...TA.G.....T..A.....A	2100

FIG. 2F

MAJORITY	AGCTTCCCCAAGGTGCGGGCCTGGATTGAGAAAGACCCTGGAGGAGGCGAGGCGGGGTACGTGGAGA	
DNAPTAQ	2164
DNAPTFL	...A.....GG.....C.....C.CC.....T.....	2161
DNAPTTHA.A.....G.....A.....C.....A.....	2170
MAJORITY	CCCTCTTCGGCCGCCGGCTACGTGCCCCGACCTCAACGCCCGGGTGAAGAGCGTGCGGGAGGCGGCGGA	
DNAPTAQC.....A.....AG.G.....C...	2234
DNAPTFLT.....C.....C.....	2231
DNAPTTHAA.AA.....CA.....C.....	2240
MAJORITY	GCGCATGGCCTTCAACATGCCCCGTCCAGGGCACCGCCGCCGACCTCATGAAGCTGGCCATGGTGAAGCTC	
DNAPTAQG.....T.....T.....	2304
DNAPTFLG.....CG...T	2301
DNAPTTHC.....C.....	2310
MAJORITY	TTCCCCCGGCTXCAGGAAATGGGGGCCAGGATGCTCCTXCAGGTCCACGACGAGCTGGTCTCGAGGGCCC	
DNAPTAQA...GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTHC.C.G...G.....C.C.....C.....G.....	2380
MAJORITY	CCAAAGAGCGGGCGGAGGXGGTGGCCCGCTTTGGCCAAGGAGGTCTATCCCCCTGGCCGT	
DNAPTAQ	A.....A.....CC.....CGGC.....G.....	2444
DNAPTFL	...G.C.....AG...A.....GG.....CAG..	2441
DNAPTTH	.C...C.....C...A.....G.....C.....AA..C.....C.....	2450

FIG. 2G

MAJORITY	GCCCCCTGGAGGTGGAGGTGGGGATGGGGGAGGACTGGCTCTCCGCCCAAGGAGTAG	
DNAPTAQA.....	2499 GA
DNAPTFLCC.....	2496
DNAPTTHT.....GT...	2505

FIG. 2H

MAJORITY		MXAMLPLFEPKGRVLLVDGHHLAYRTFFALKGLTTSRGEVPQAVYGFAKSLKALKEDG·DAVXVVFDK	
TAD PRO	.RG.....	H.....	69
TFL PROI.....	68
TTH PRO	E.....V.V.....	70
		YK..F.....	
MAJORITY		APSRHEAYEAYKAGRPTPEDFPROLALIKELVDLLGLXRLEVPGYEADDVLATLAKKAEKEGYEVRIL	
TAG PROGG.....A.....S.....	139
TFL PROV.....F.....R.....	138
TTH PROFT.....	140
MAJORITY		TADRDLYQLLSDRIAVLHPEGYLITPAWLWEKYGLRPEQWVDYRALXGDPNDLPGVKGIGECTAXKLLX	
TAG PROK.....H.....D..A.....T..E.....R...E	209
TFL PROE...I.....Y.....A.....I.....QR..IR	208
TTH PROV...V.....H...E.....F..V.....L...K	210
MAJORITY		EWGSLLENLLKNLDRVKP·XXREKIXAHMEDLXLSXXLSXVRTDLPLEVDFAXRREPDREGLRAFLEF	
TAG PROA.....L...AI...L...D..K..WD.AK.....K.....R.....	278
TFL PROFQH...Q...SL...LQ.G..A.A..RK..Q.H.....GR..T.NL.....	277
TTH PROENV.....K..L...R..LE..R.....L.QG.....	280
MAJORITY		GSLLEFGLLXPKALEEAPWPPPEGAFVGFVLSRPEPMWAEALLALAAARXGRVHRAXDPLXGLRDLKEV	
TAG PROS.....K.....D.....PE.YKA.....A	348
TFL PROG...A.....L..SF.....G.WE..L...Q...R.....G.	347
TTH PROA.AP.....K.....C.D.....A...A..K.....	350

FIG. 3A

MAJORITY		RGLAKDLAVLALREGLDLXPGDDPMLLAYLLDPSNTTPEGVARRYGGWETEDAGERALLSERLFXNLXX	
TAQ PROS.....G.P.....E.....A.....A.....WG	418	
TFL PRO	..I.....F.E.....A.....QT.KE	417	
TTH PROS.....V.....AH.....HR..LK	420	
MAJORITY		RLEGEERLLWLXYEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRLEEVEFRLAGHPFNLNSRD	
TAQ PROR...R...A.....R.....A.....A.....	488	
TFL PRO	..K.....E.....R.....EA.V.Q.....	487	
TTH PROK.....H.....L.....	490	
MAJORITY		QLERVLFDELGLPAIGKTEKTKGRSTSAAVLEALREAHPIVEKILQYRELTKLKNTYIDPLPXLVHPRTG	
TAQ PRO0	558	
TFL PRODR.....S.....D.I.....	557	
TTH PROR...L...Q.....H.....V.....S.....	560	
MAJORITY		RLHTRFNQTATATGRLSSSDPNLQNIPTPLGQRIIRRAFVAEEGWXLVALDYSQIELRVLAHLSGDENL	
TAQ PROI.....L.....	628	
TFL PROV.V.....	627	
TTH PROA.A.....	630	
MAJORITY		IRVFQEGRDIHTQTASWMFGVPPEAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPIYEEAVAFIERYFQ	
TAQ PROE.....R.....Q.....	698	
TFL PROS.G.....G.S.....	697	
TTH PROK.....V.....	700	

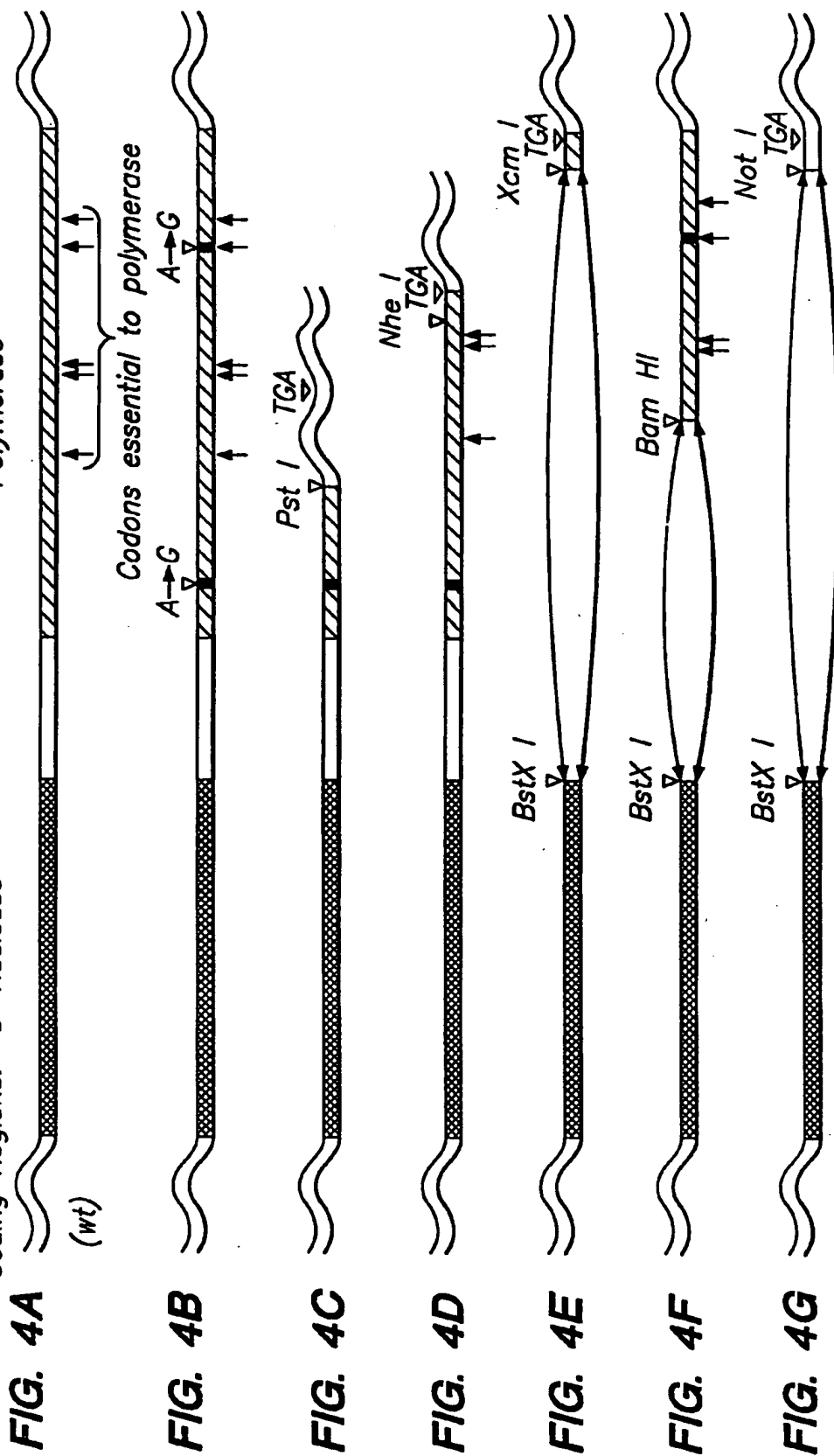
FIG. 3B

MAJORITY	SFPKVR	AWIEKT	LEEGR	RRGY	VETLF	GRRRY	VPDLN	ARVKS	VREAA	ERMAF	NMPV	QGTAA	DLMK	LAMV	KKL	
TAQ PRO	768
TFL PRO	767
TTH PRO	770
MAJORITY	FPRLX	EMGAR	MLLQ	VHDEL	VLEAP	KXRAE	XVAAL	AKEV	MEGV	YPLAV	PLEVE	VGXG	EDWL	SAKEX		
TAQ PRO	833
TFL PRO	831
TTH PRO	835

FIG. 3C

Genes for Wild-Type and Pol(-)DNAPTaq

Domain
Coding Regions: 5' Nuclease



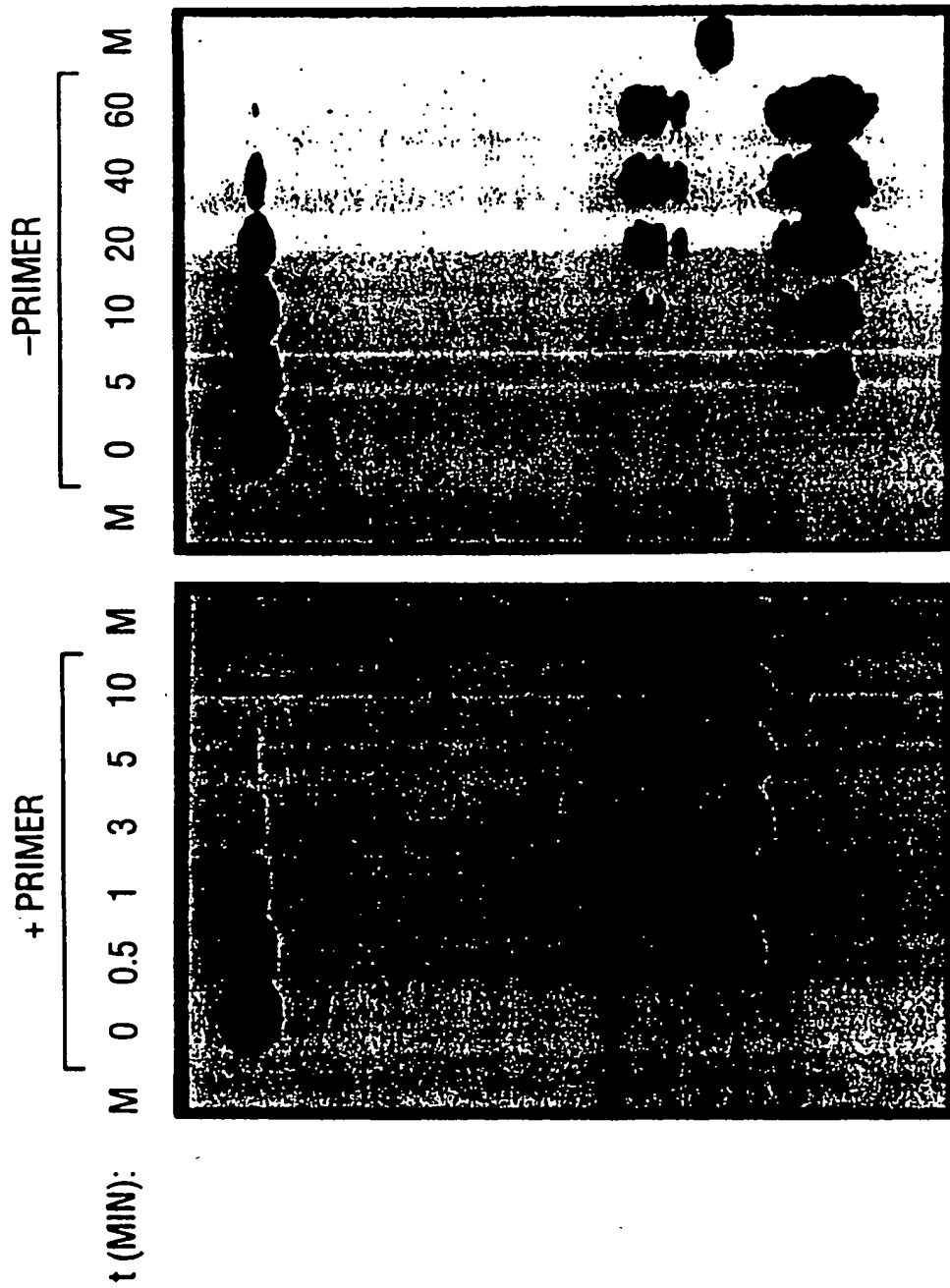


FIG. 10A

FIG. 10B



FIG. 11B

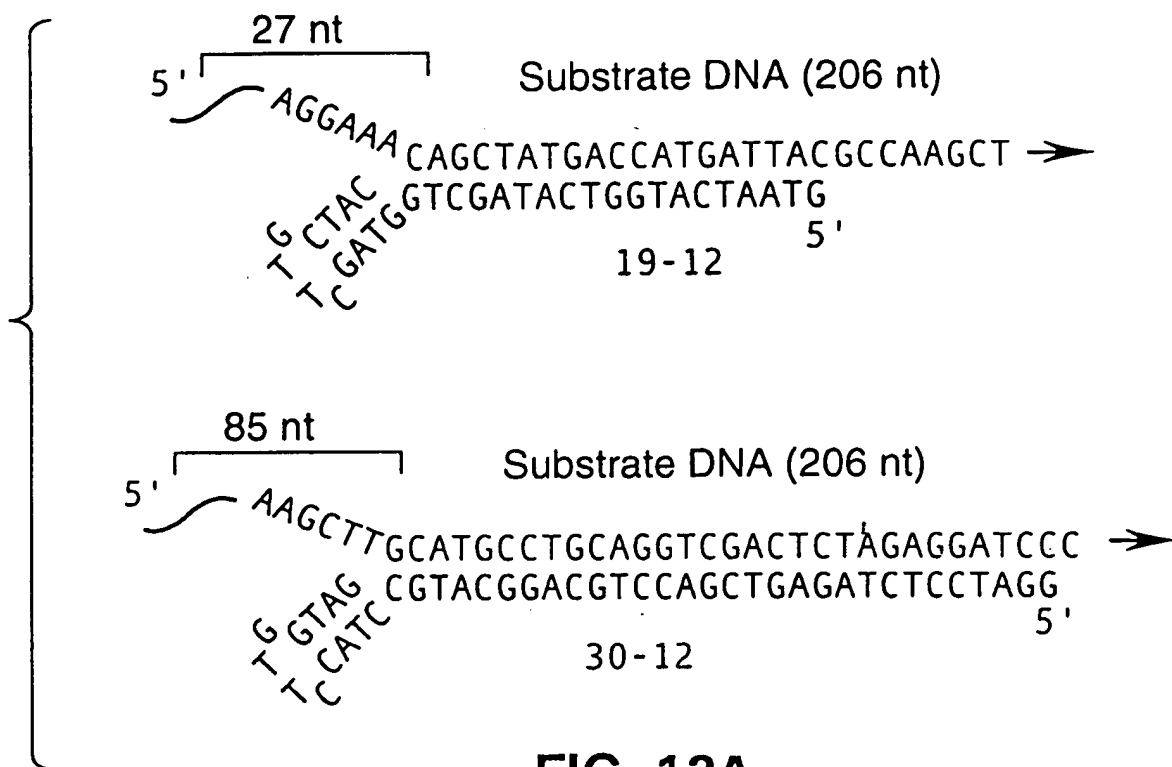


FIG. 12A

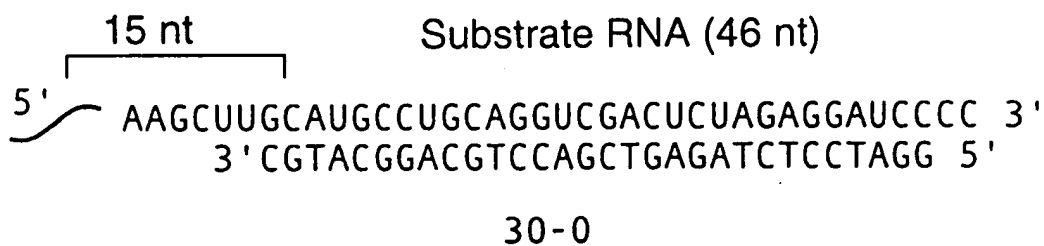


FIG. 13A

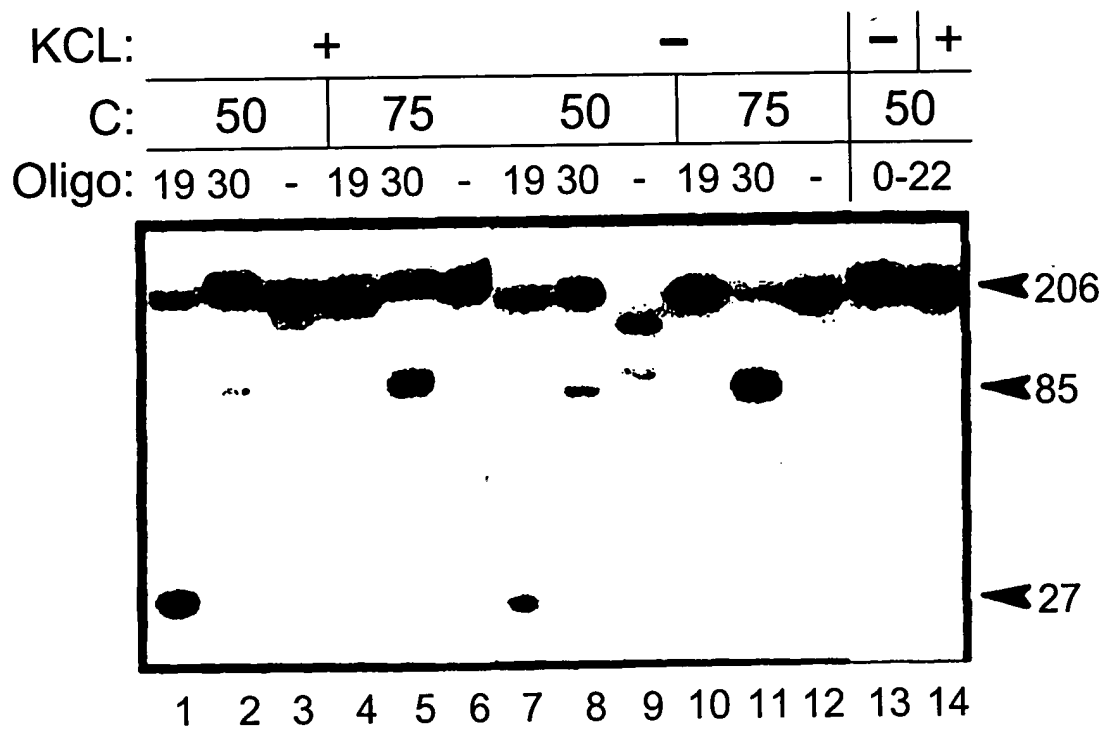


FIG. 12B

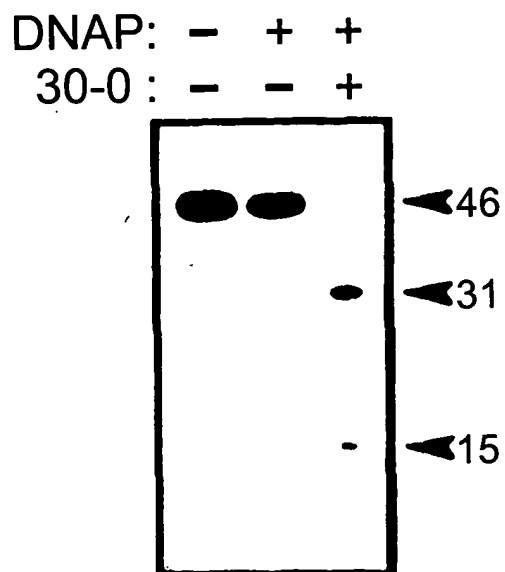
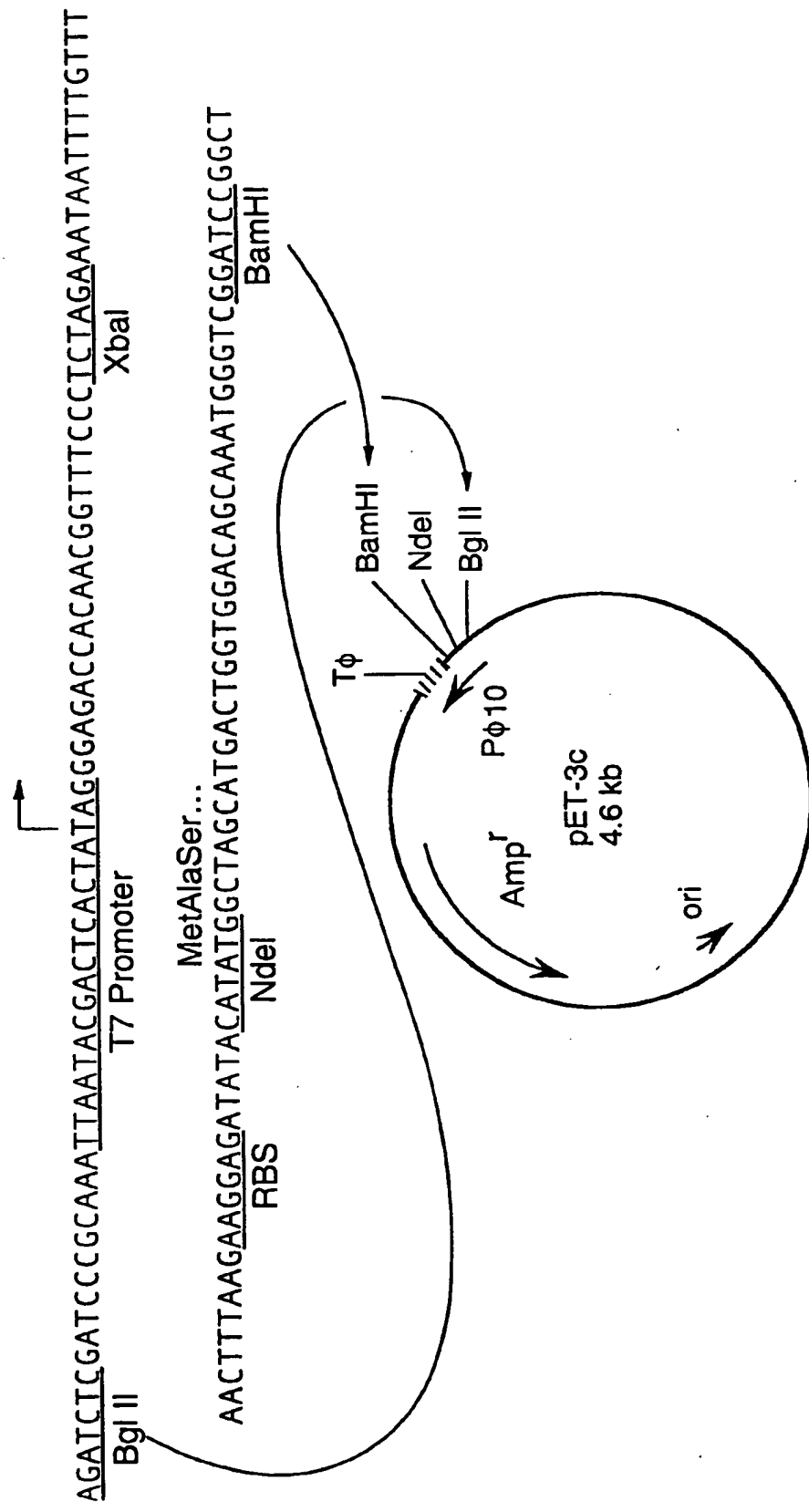


FIG. 13B



P_{φ10}: Bacteriophage T7 ϕ 10 promoter RBS: Ribosome binding site
T_φ: T7 ϕ Terminator

FIG. 15

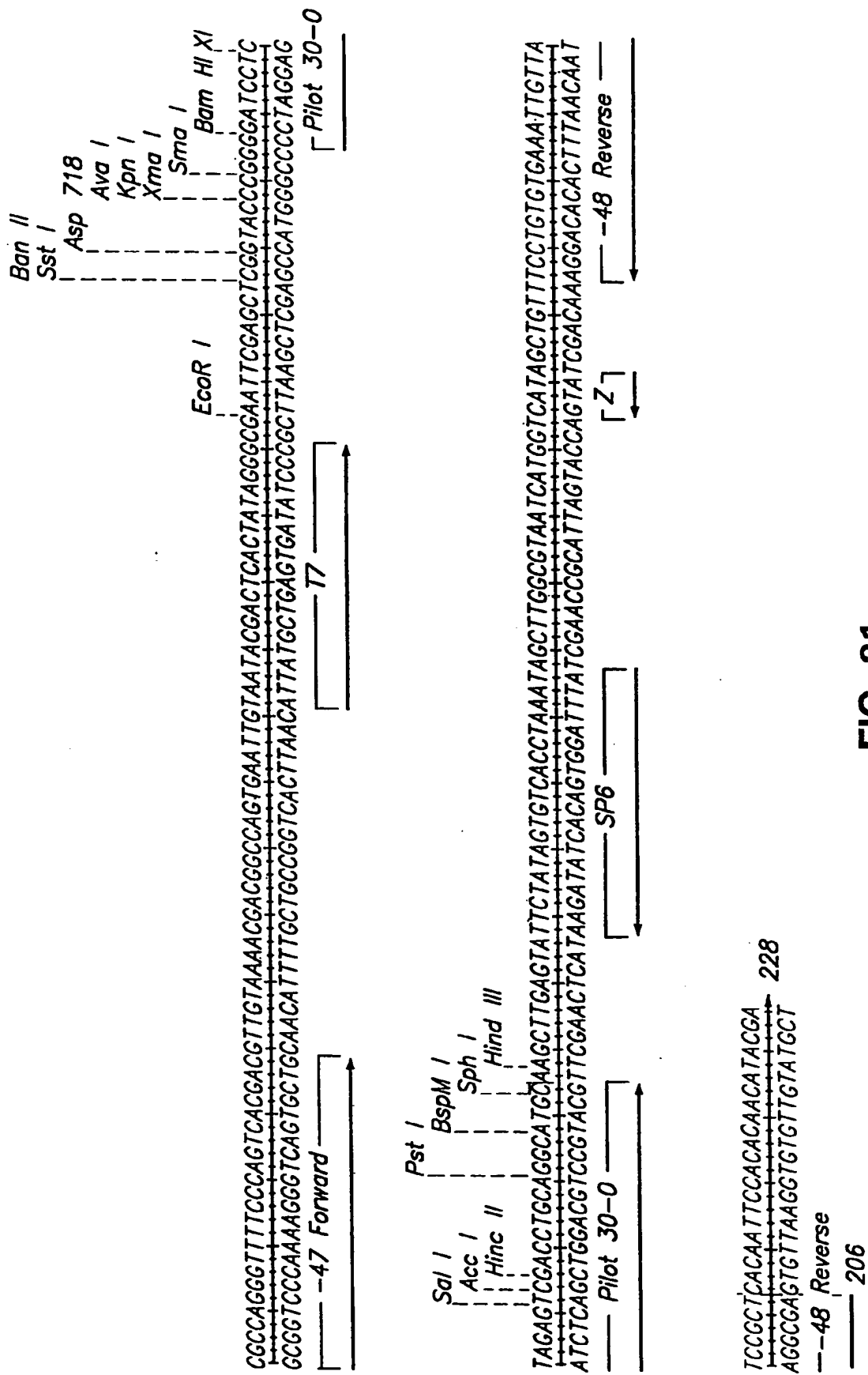


FIG. 21

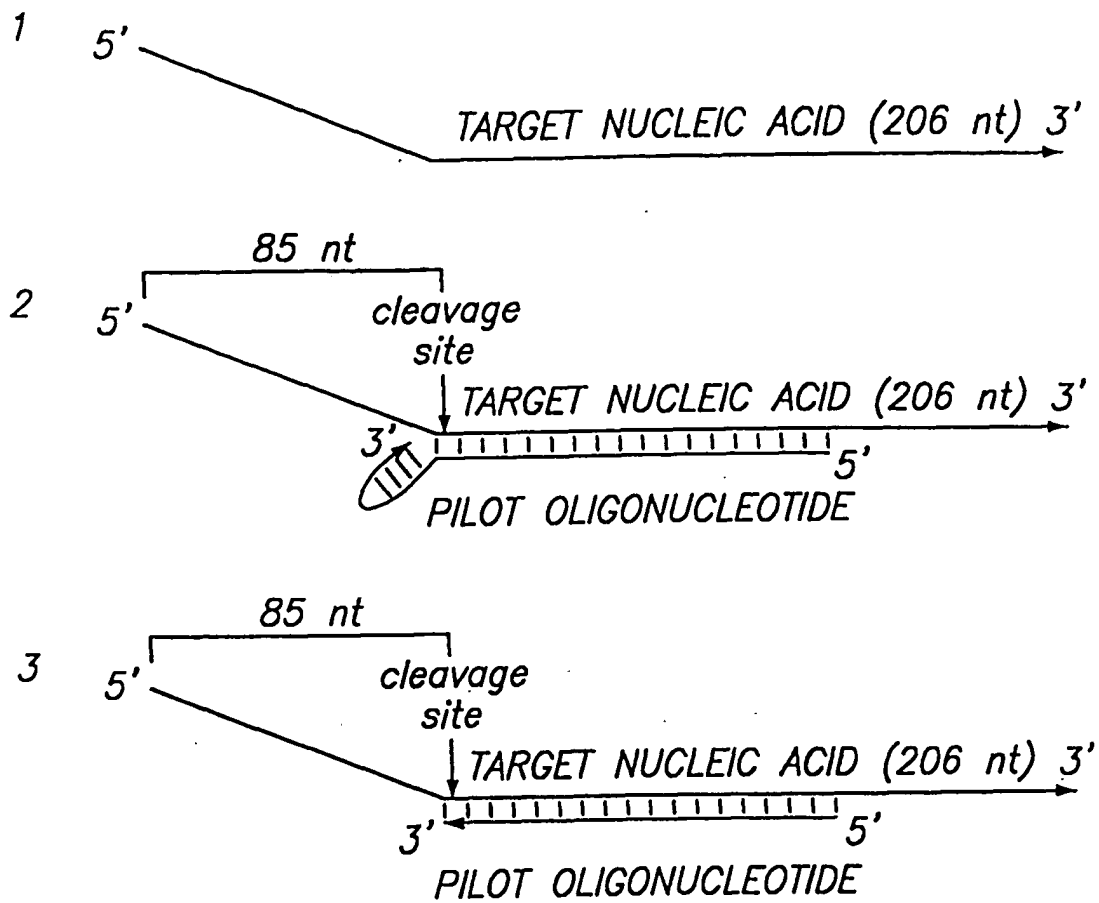


FIG. 22A

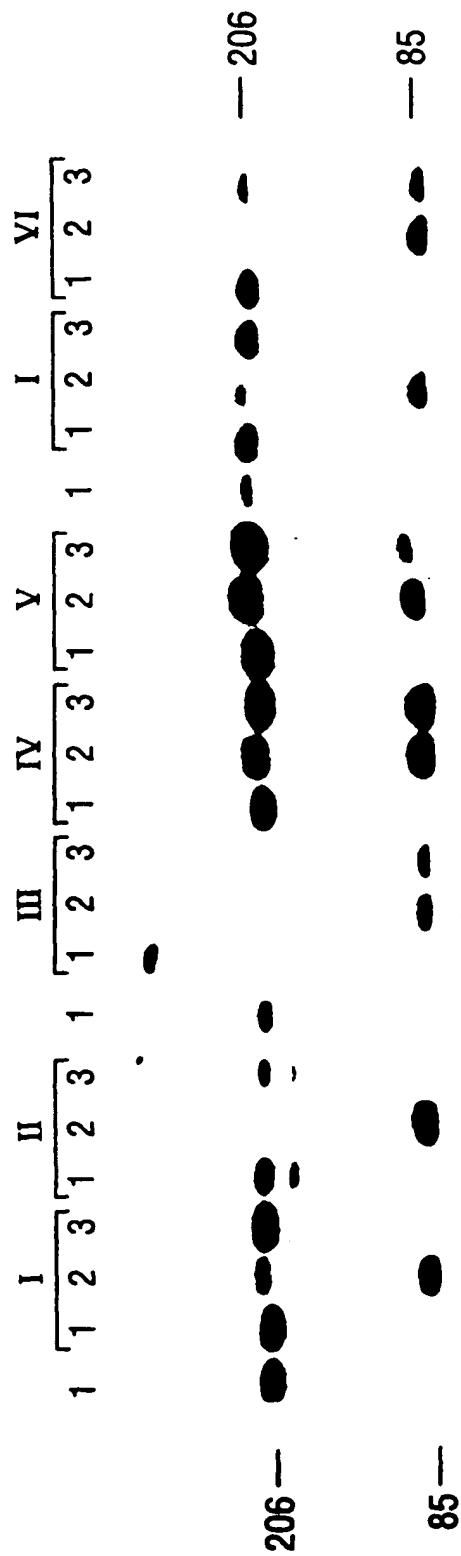


FIG. 22B

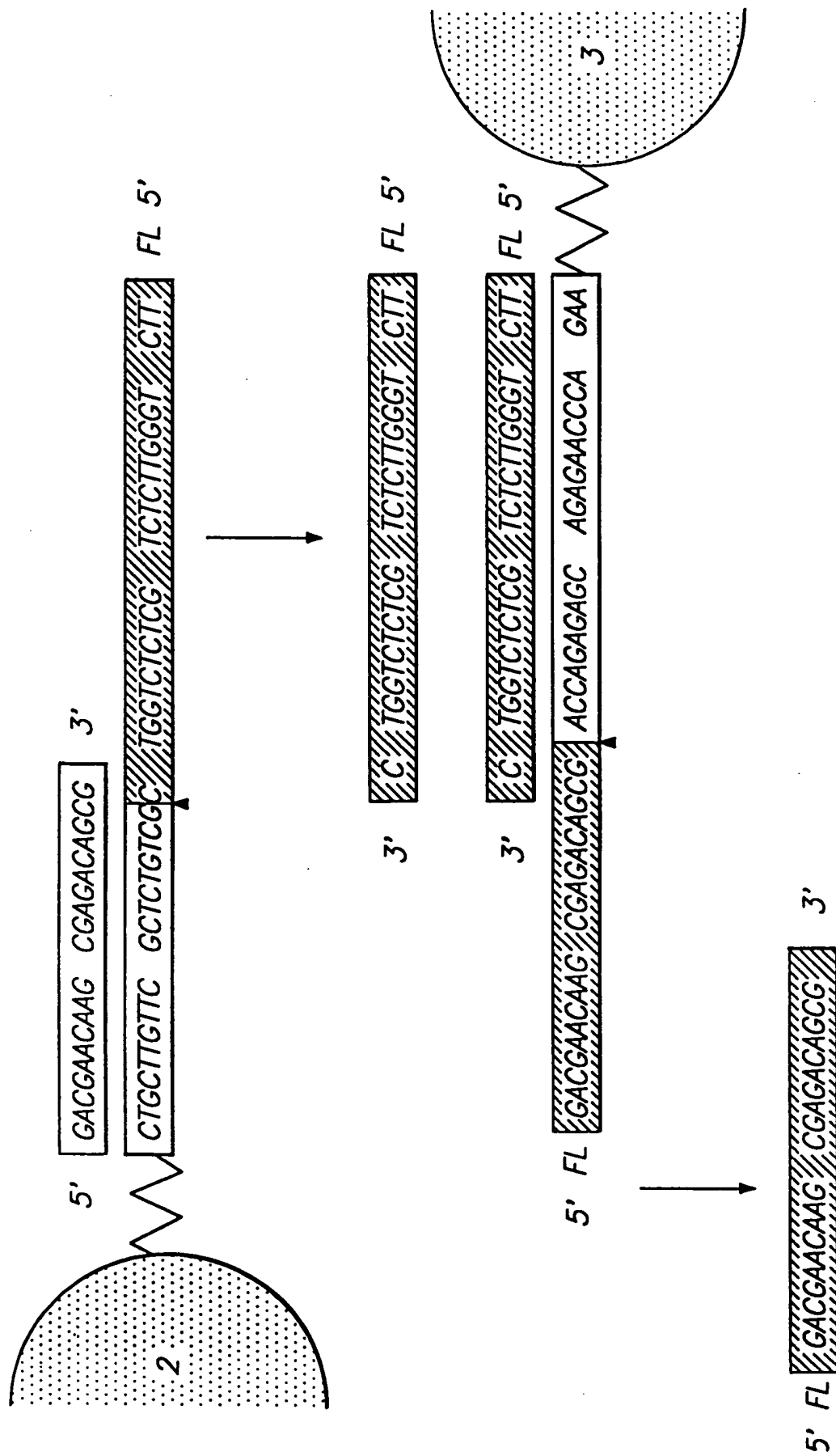


FIG. 23

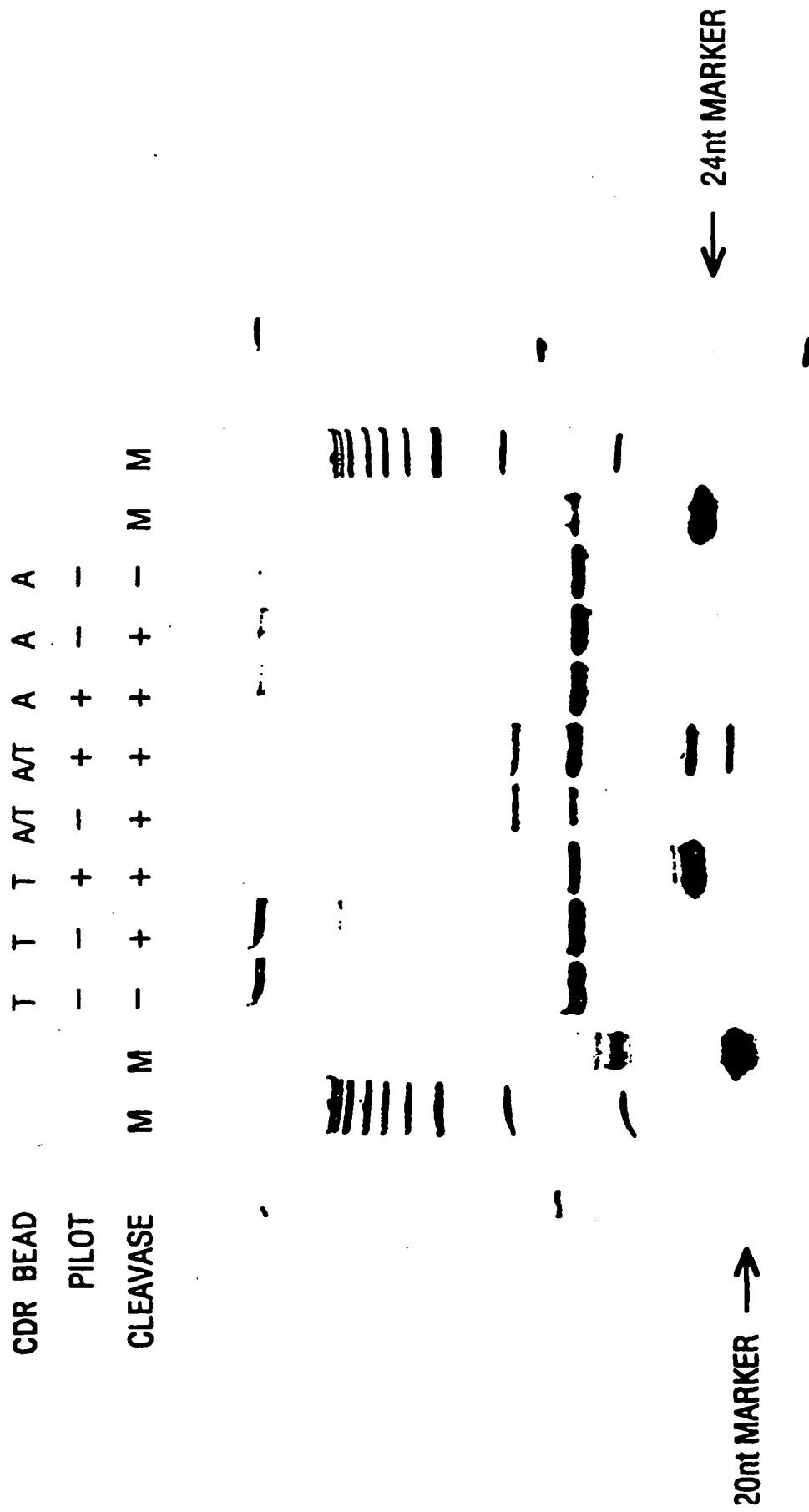


FIG. 24

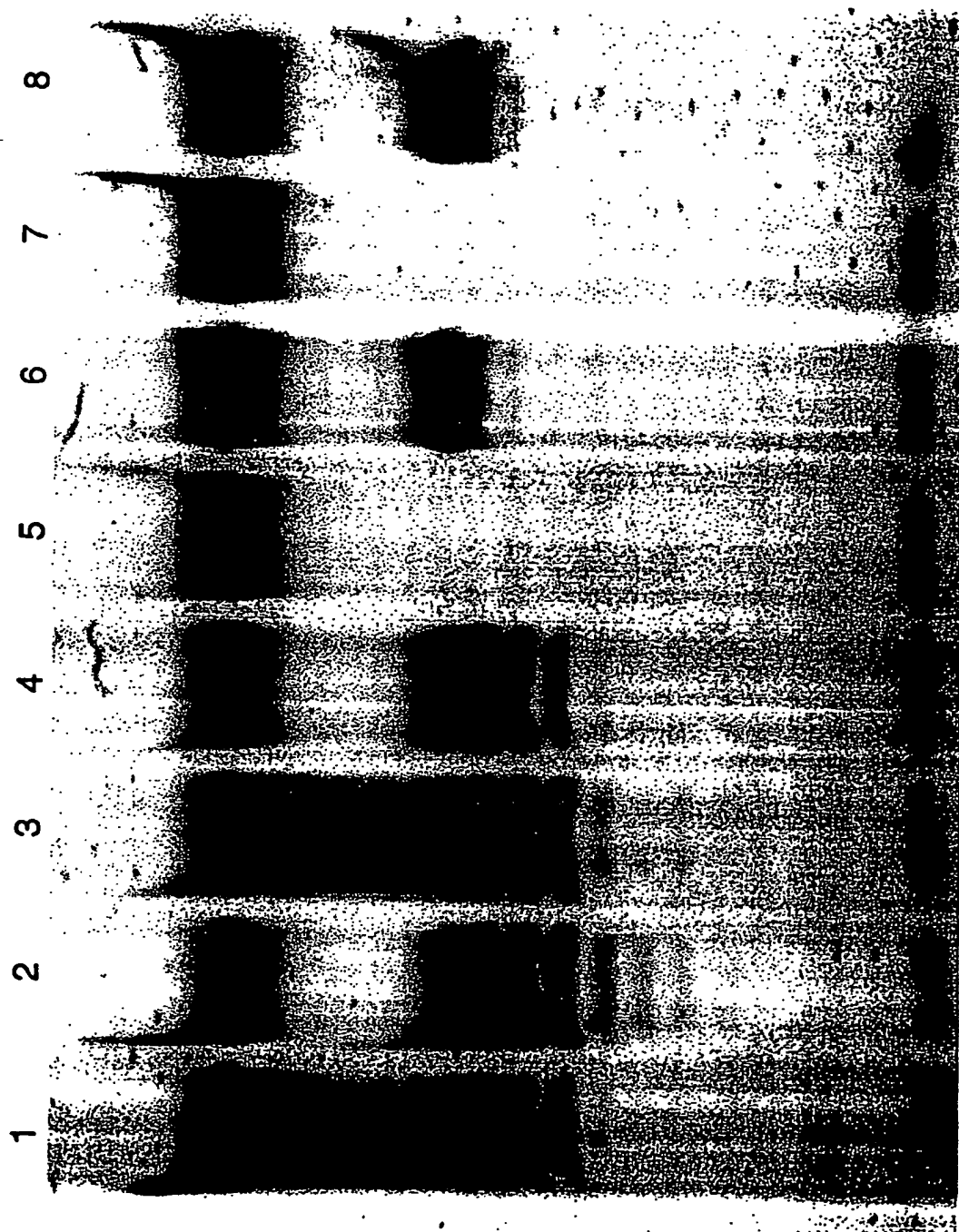
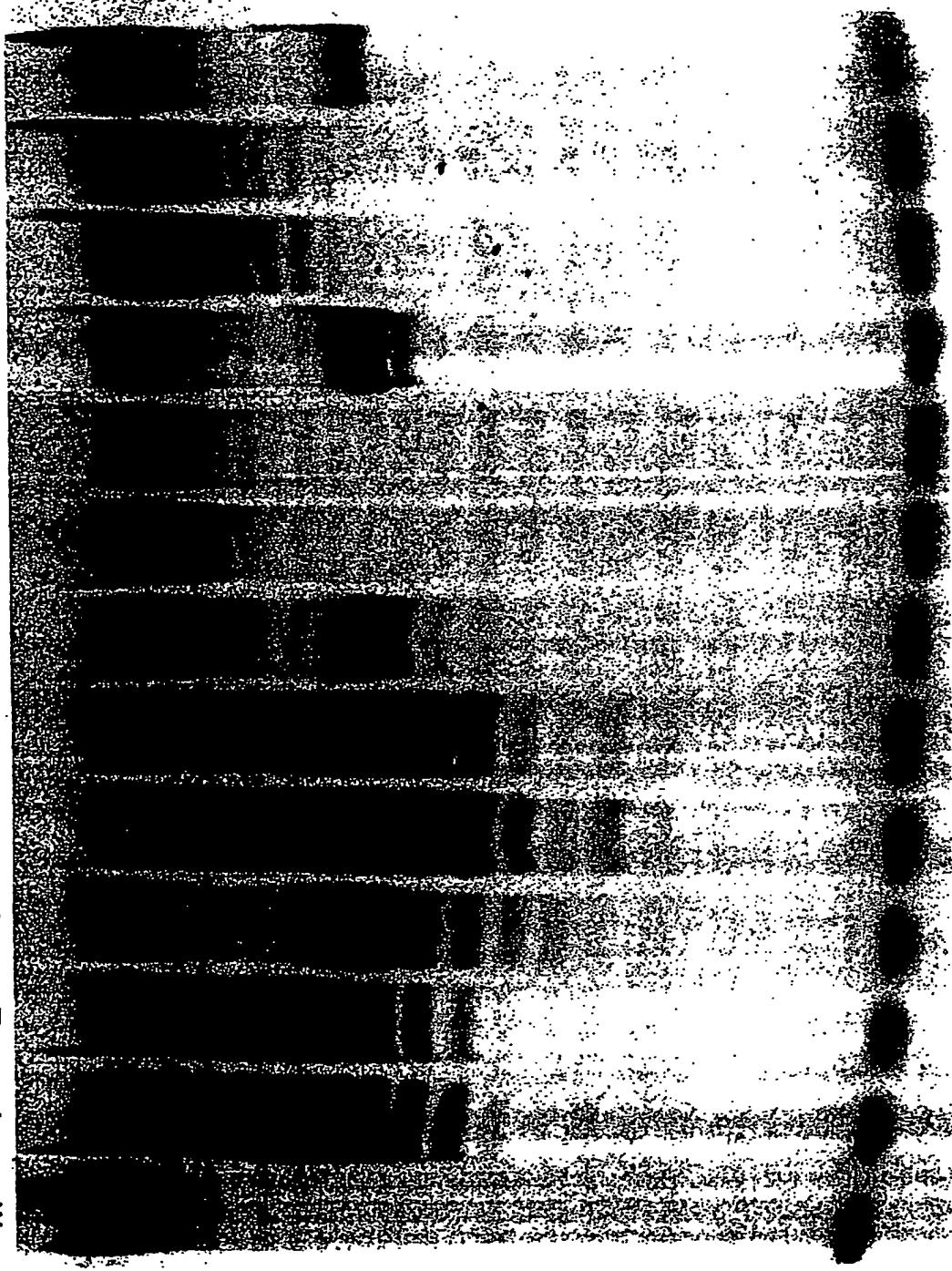


FIG. 33

M 1 2 3 4 5 6 7 8 9 10 11 12



26

FIG. 34

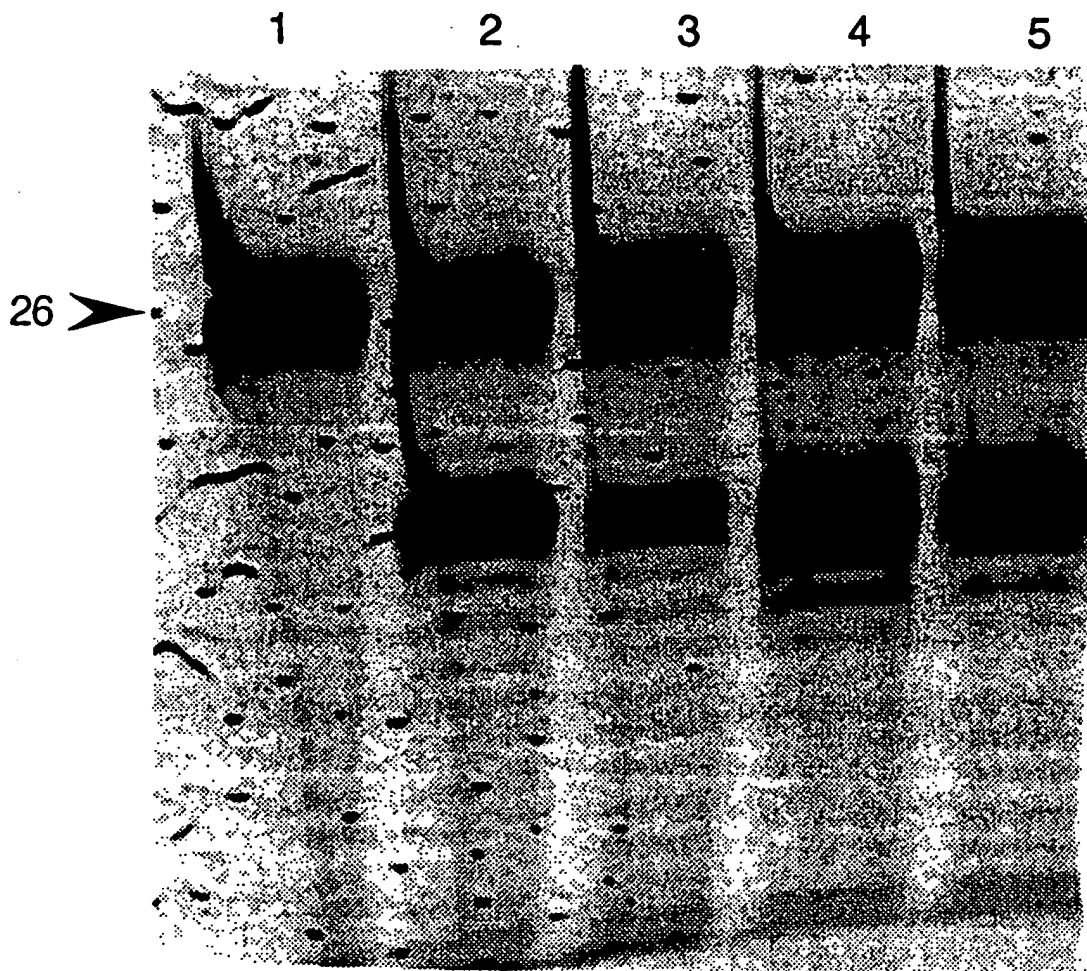


FIG. 35

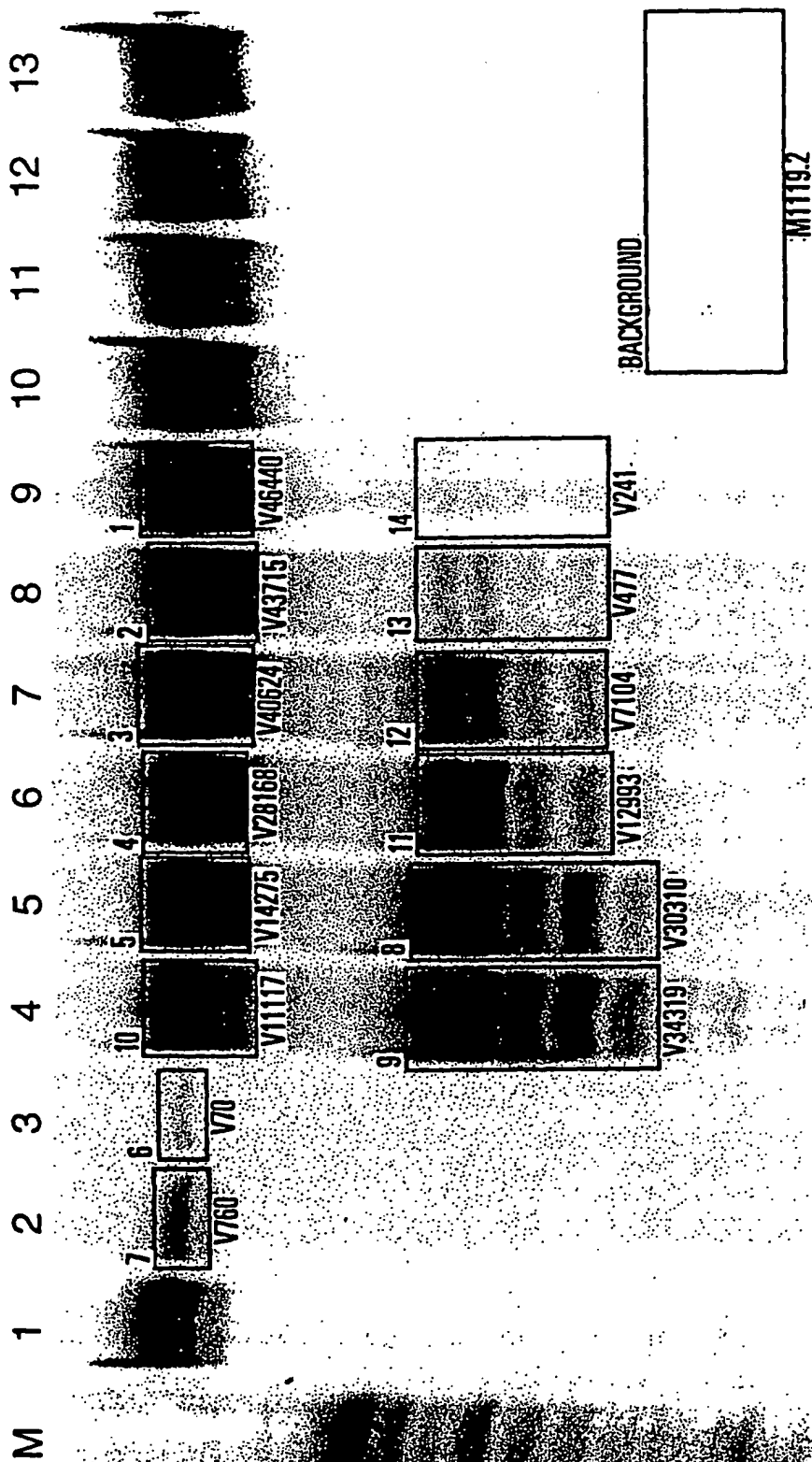


FIG. 36

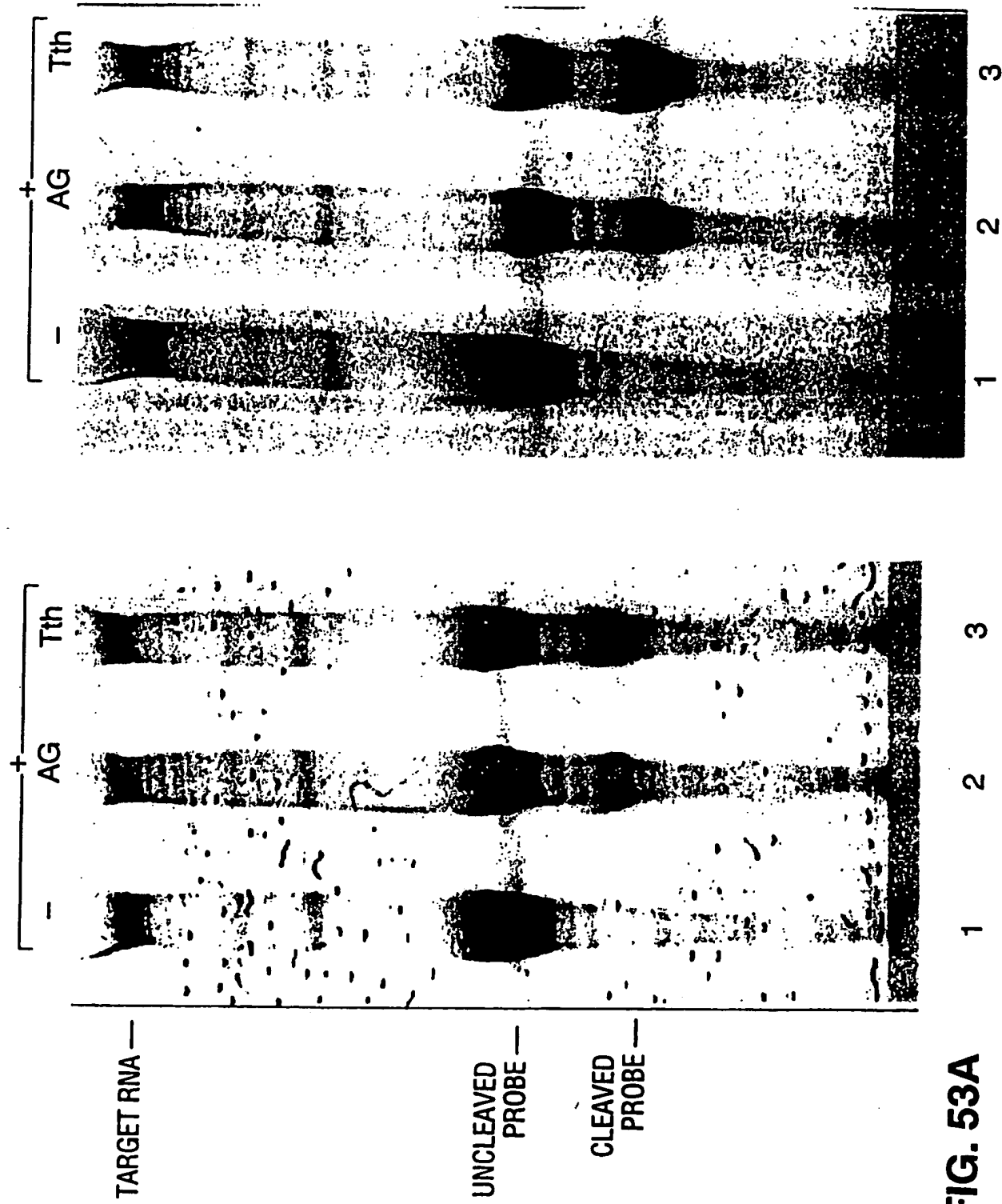


FIG. 53A

FIG. 53B

— ENZYME
— TARGET (fmol)
— RNA

500 1 5 10 50 100 100 1 5 10 50 100

CLEAVASE AG

Tth

— PROBE

— PRODUCT

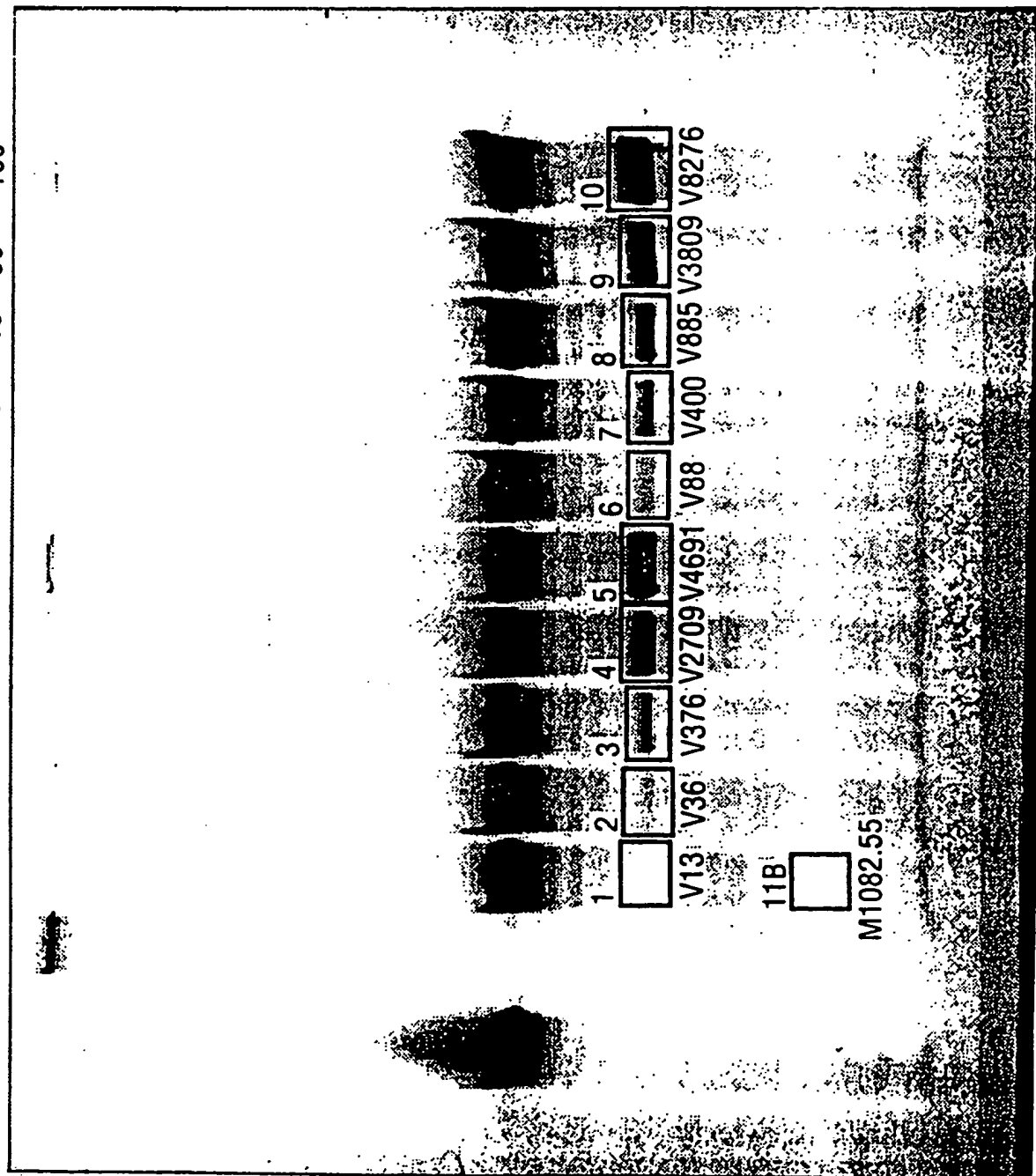


FIG. 54

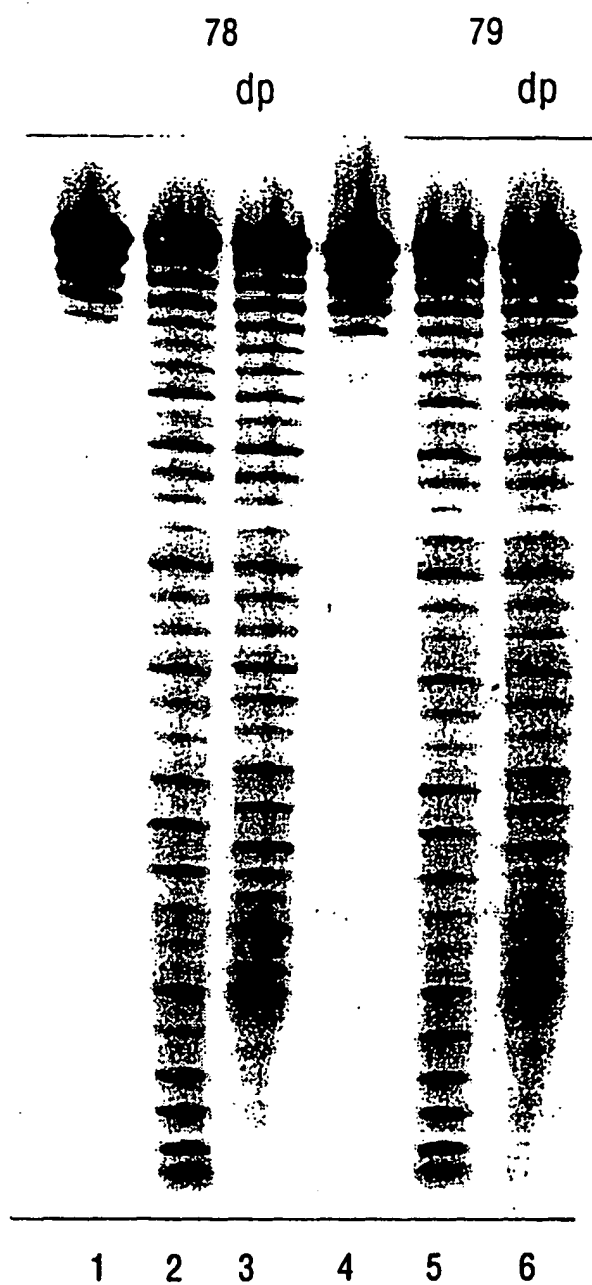


FIG. 55

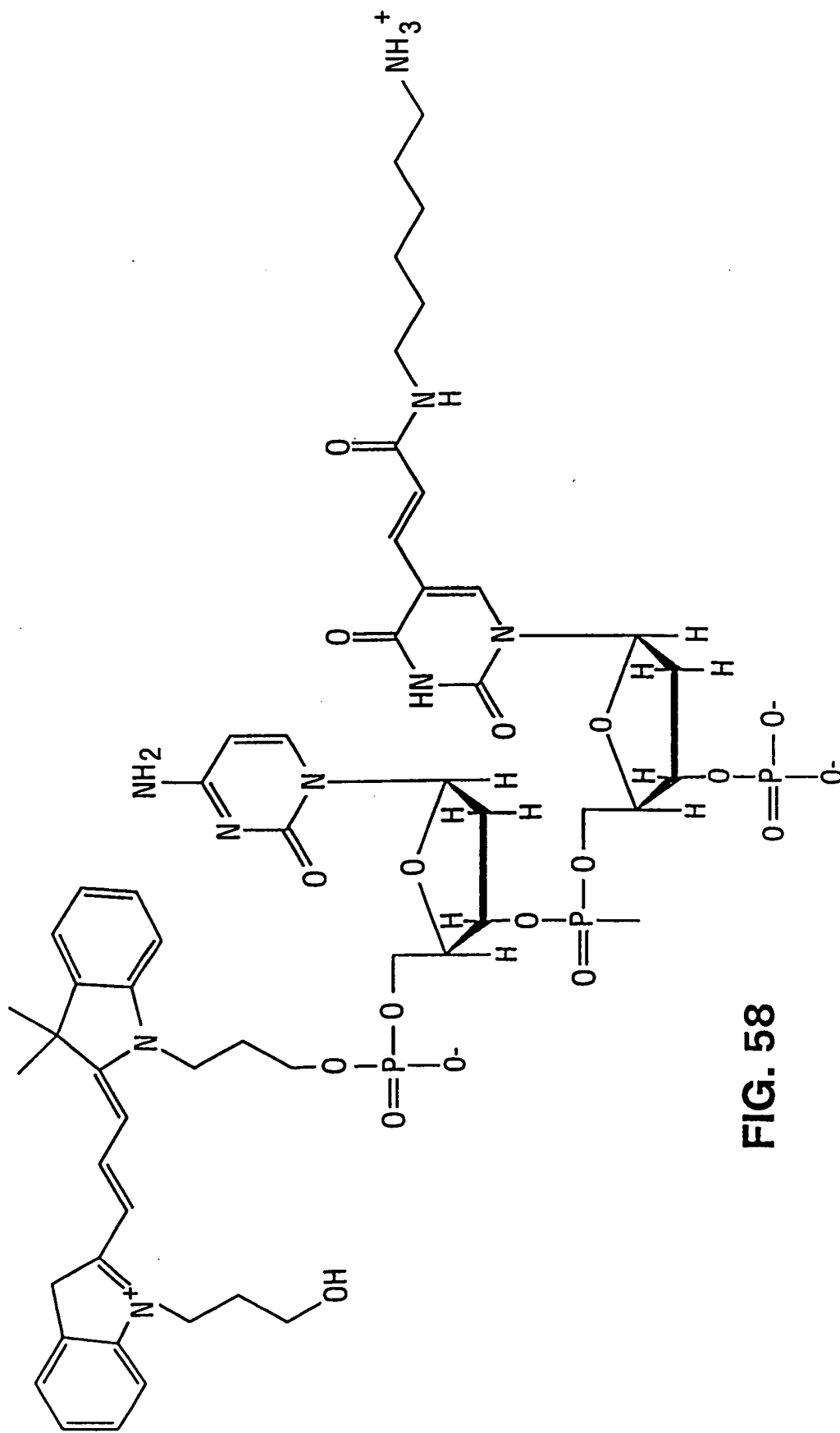


FIG. 58



FIG. 65A

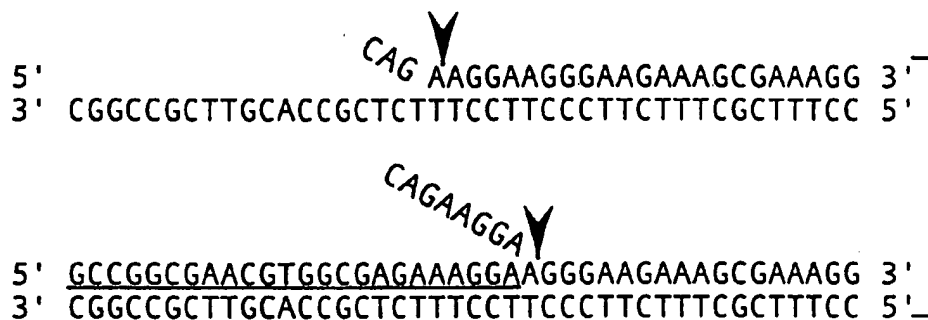


FIG. 65B



FIG. 65C

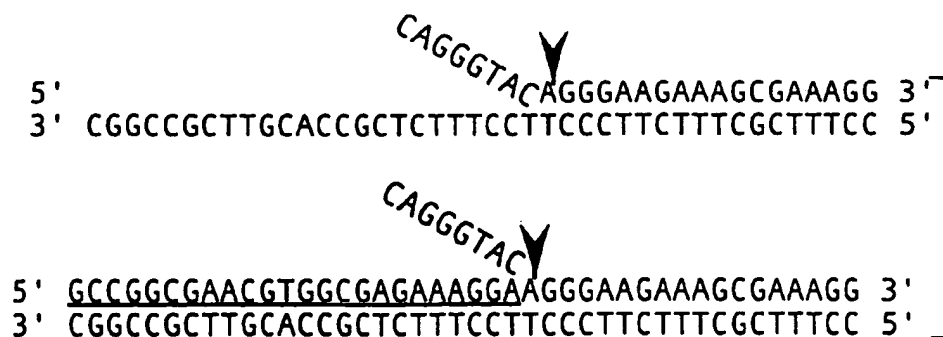


FIG. 65D

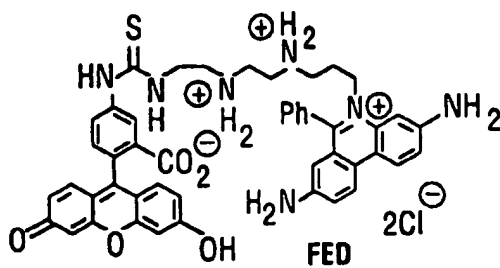
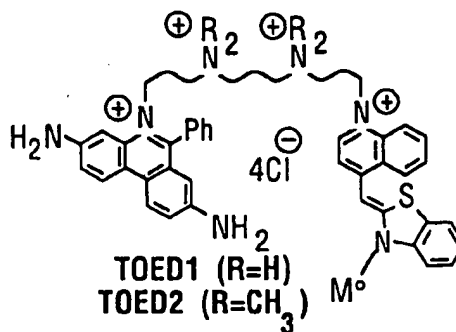
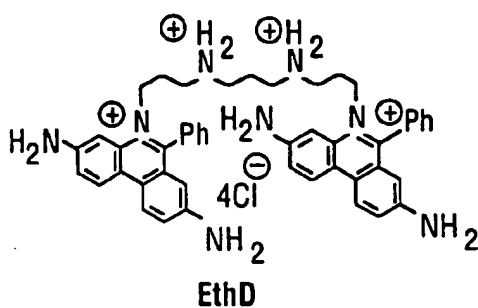
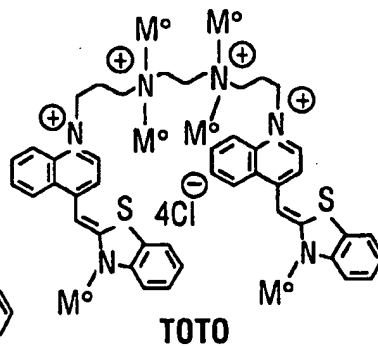
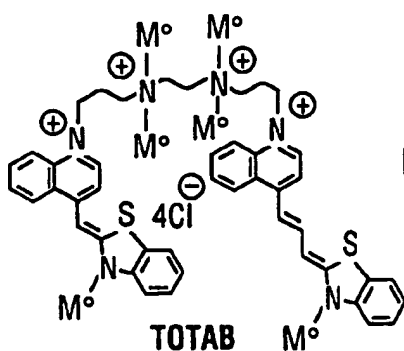
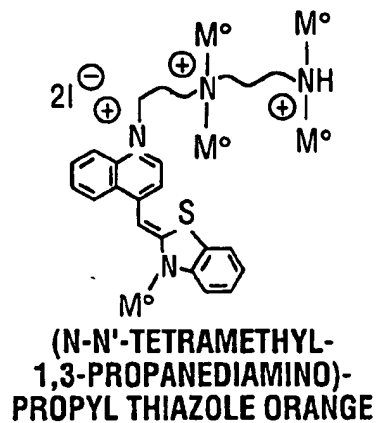
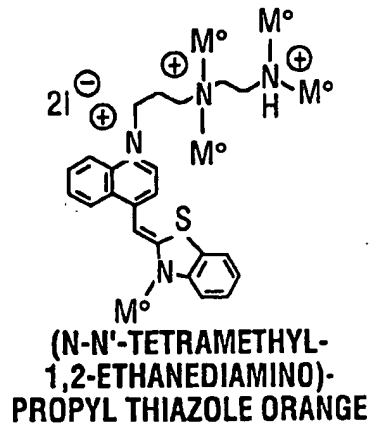
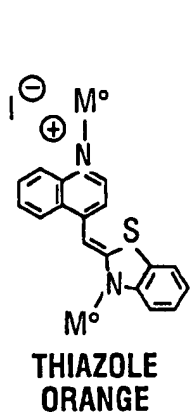
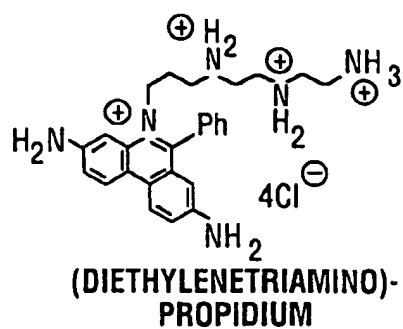
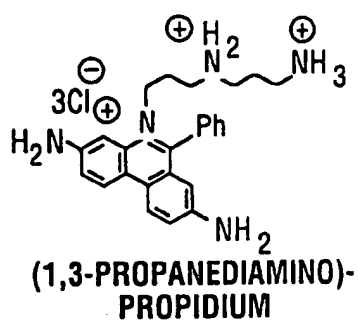
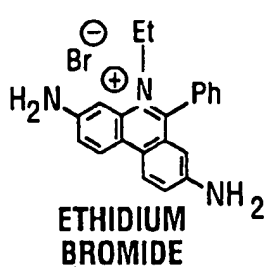


FIG. 66

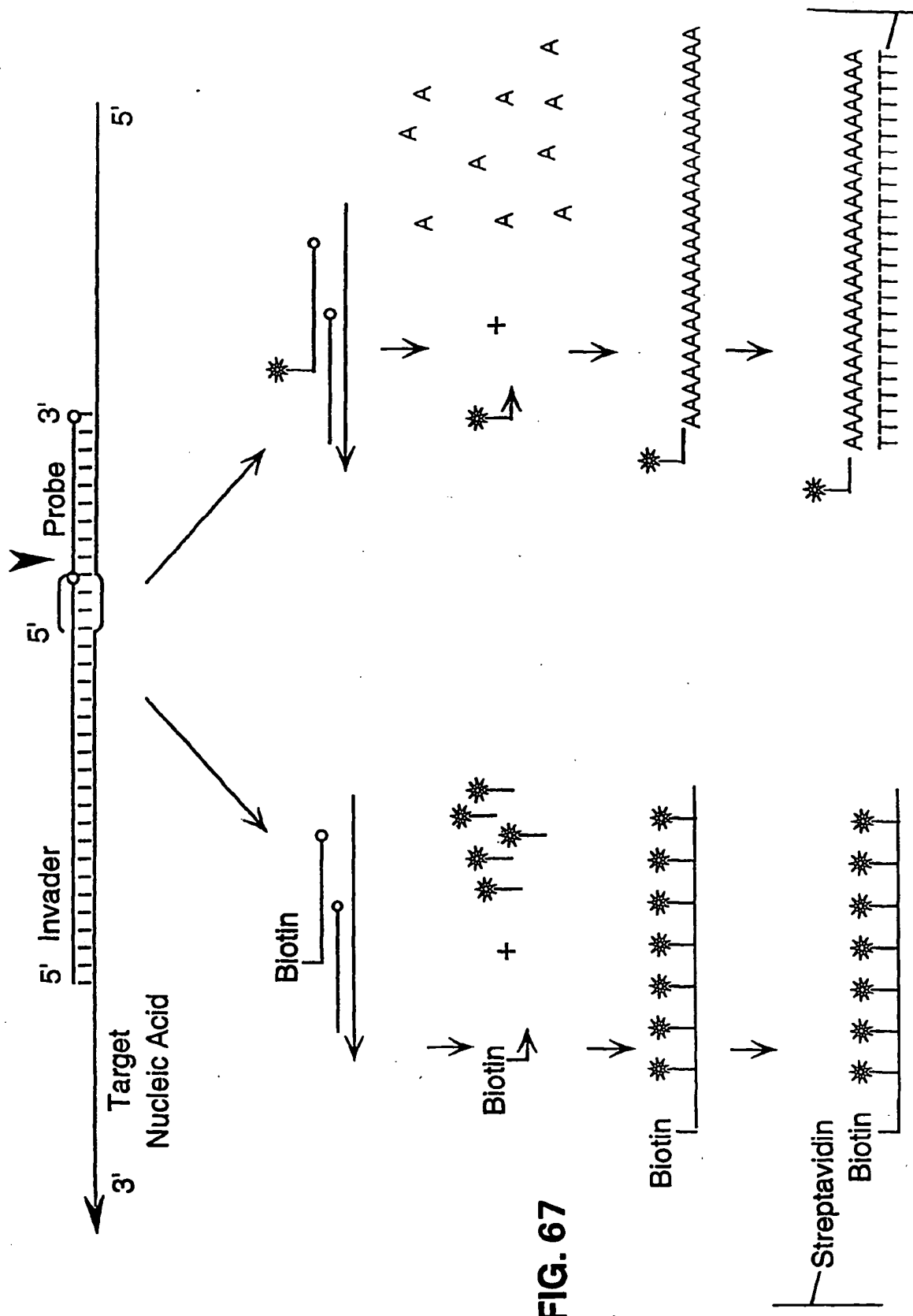


FIG. 67

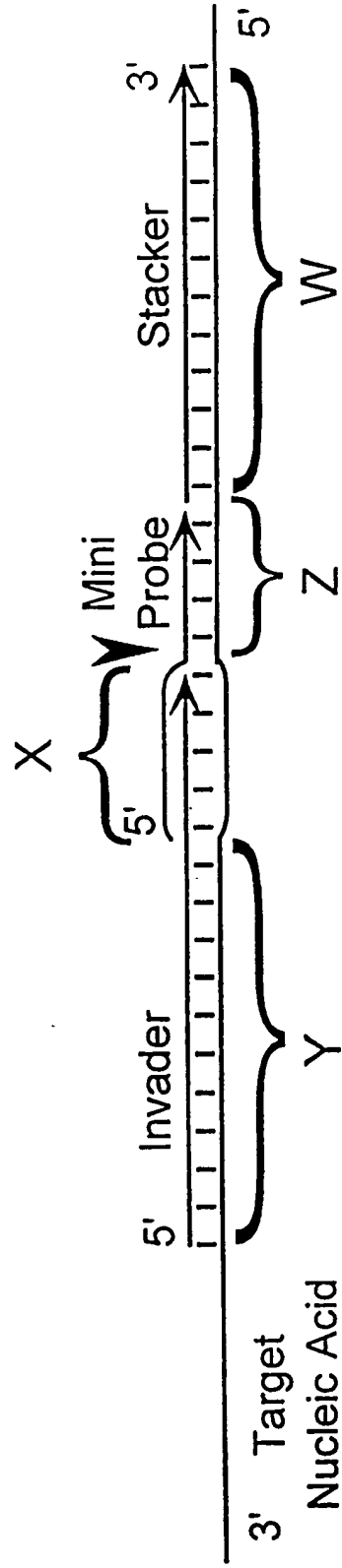


FIG. 68

	10	20	30	40	50	60	70					
1	MGVQ-----	FGDFIPK--	NIISFEDL	KGKKVAID	GMNALYQFLT	SIRLDGSP	LRNRKGEITS	AYNGVFY	MJAFEN1.PRO			
1	MGVP-----	IGEIIPR--	KEIELENL	YGKKIAID	ALNAIYQFL	STIRQKDG	TPLMDSKGR	ITSHLSGLFY	PFUFEN1.PRO			
1	MGIQGLAK	LIADVAPSA	IRENDIKSY	FGRKVAID	ASMSIYQFL	IAVRQ--GGD	VLQNEEGETT	SHLMGMFY	HUMFEN1.PRO			
1	MGIHGLAK	LIADVAPSA	IRENDIKSY	FGRKVAID	ASMSIYQFL	IAVRQ--GGD	VLQNEEGETTS-	LMGMFY	MUSFEN1.PRO			
1	MGIKGLNA	IISEHVPSA	IRKSDIKS	FFGRKVAID	ASMSLYQFL	IAVRQDGG	QLTNEAGETT	SHLMGMFY	YST510.PRO			
1	MGVHSFWD	IAG----	PTARPVR	LESLEDK	RMADASI	WIYQFLK	AVRDQEGNA	VKN-----	SHITGFFR	YSTRAD2.PRO		
1	MGVSGLWN	ILE----	PVKRPVK	LETLVN	KRLAID	ASIWIYQFL	KAVRDKEGN	QLKS-----	SHVVGFFR	SPORAD13.PRO		
1	MGVQGLWK	LLE----	CSGROVS	PEALEG	KILAVD	ISIWL	NQALKGVRD	RHGS	SIEN-----	PHLLTLFH	HUMXPG.PRO	
1	MGVQGLWK	LLE----	CSGHRVS	PEALEG	KVLAVD	ISIWL	NQALKGVRD	SHGN	VIEN-----	AHLLTLFH	MUSXPG.PRO	
1	MGVQGLWK	LLE----	CSGRP	INPGT	LEGKIL	AVDISI	WL	NQAVKGARD	RQGN	AIQN-----	AHLLTLFH	XENXPG.PRO
1	MTINGIWE	WANHVV----	RKVPNET	MRDKT	LSIDGHI	WLYESL	KGCEA	HHQQT-----	PNSYL	VTFFT	CELRAD2.PRO	

	80	90	100	110	120	130	140						
64	KTIHLL	ENDITPIW	VDGEP	PKLKEK	TRKVR	REMKEA	ELKMKEAIKK----	EDFEEAAKYAKRVS	YLTP	MJAFEN1.PRO			
64	RTINL	MEAGIKP	VYVFDG	EPPEFK	KKKELE	KRRREAR	EEAEKWR	EALEK----	GEIEEARKYAQRATRVNE	PFUFEN1.PRO			
70	RTIRM	MENGIKP	VYVFDG	KKPPQL	KSGLAK	RSERRAE	AEKQLQQA	AA----	GAEOEVEKFTKRLVKVTK	HUMFEN1.PRO			
69	RTIRM-	ENGIKP	VYVFDG	KKPPQL	KSGLAK	RSERRAE	AEKQLQQA	QEAE----	GMEEEVEKFTKRLVKVTK	MUSFEN1.PRO			
71	RTIRM	IDNGIKP	CYVFDG	KKPPDL	KSHEL	TKRSSRR	VETEK	KLAE----	EA-----	TTELEKMKQERRLVKVSK	YST510.PRO		
61	RICKLL	YFGIRP	VVFDG	GVPLK	RETIRQ	KERRQ	KGKRESA	KSTARK	LALQLQ	NGSNDNKRDSDEVTM	YSTRAD2.PRO		
61	RICKLL	FFGIRP	VVFDG	GGAPSL	KRQTIQ	KRQARRL	DREENAT	VTANK	LLALQMR	HQAMLKRDADEV	TQ	SPORAD13.PRO	
61	RLCKLL	FFRIRP	IFVFDG	DAPLLK	KQTLV	KRRQRK	DASSDS	SRKTT	EKLLK	TFLKRQA	IKTERIAA	VTG	HUMXPG.PRO
61	RLCKLL	FFRIRP	IFVFDG	DAPLLK	KQTLA	KRRQRK	DSASID	SRKTT	EKLLK	TFLKRQA	LKTDRIA	ASVTG	MUSXPG.PRO
61	RLCKLL	FFRIRP	IFVFDG	EAPLLK	RQTLA	KRRQR	TDKASND	ARKTNE	KLLRT	FLLKRQA	IKAERIA	AATVTG	XENXPG.PRO
60	RIQRLL	LELKII	PIVVDN	INASSA	HESKDQ	NEFVPR	KRRSFG	DSPTNLV-----	-----	-----	-----	-----	CELRAD2.PRO

FIG. 70A

	150	160	170	180	190	200	210
130	KMVENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLT	TTTKEM----					MJAFEN1.PRO
130	MLIEDAKKLLLELMGIPIVQAPSEGEAQAAAYMAAKGSVYASASQDYDSLFLGAPRLVRNL	TITGKRKLPGK					PFUFEN1.PRO
136	QHNDECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHL	TASEAKKLPIQ					HUMFEN1.PRO
134	QHNDECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHL	TASEAKKLPIQ					MUSFEN1.PRO
134	EHNEEAQKLLGLMGIPYIIAPTEAEQAELAKKGVYAAASEDMDTLCYRTPFLLRHL	TFSEAKKEPIH					YST510.PRO
131	DMIKEVQELLSRFGIPYITAPMEAEQAELQLNLVDGIITDSDVFLFGGKIYKNMFHEKNY	----					YSTRAD2.PRO
131	VMIKECQELRLFGIPYIVAPOEAEQAELKLEKLVGDIVTDDSDVFLFGGTRVYRNMFNQNK	F----					SPORAD13.PRO
131	QMFLESQELRLFGIPYIQAPMEAEQAELDLTDQTSGTITDSDIWLFGARHVYRNMFNQNK	F----					HUMXPG.PRO
131	QMFLESQELRLFGVPYIQAPMEAEAOCAVLDSLQTSGTITDSDIWLFGARHVYKFNKNKF	----					MUSXPG.PRO
131	QMCLESQELQLFGIPYIVAPMEAEQAELDLTDQTSGTITDSDIWLFGARHVYKFNFSQNK	H----					XENXPG.PRO
111	DHVYKTNALLTELGIKVIAPGDGEAQCARLEQLGVTSGCITTDYFLFGGKNLYRFDFTAGT	-----					CELRAD2.PRO

	220	230	240	250	260	270	280
195	-----	PELIELNEVLEDLRISLDDLIDIAIFMGTDYNPGGV--K--	GIGKRAYELVRSGVAK--DV				MJAFEN1.PRO
200	NVYVE-IKPELIILEEVLKELKLTREKLIELAILVGTDYNPGGI--K--	GIGLKKALEIVRHSKDPLAKF					PFUFEN1.PRO
206	EFHLSRILQELGLNQEVDLCIILGSDYCESIRGIGPKRAVDLIQK--	HKSIEEIVRRLDPN----	KY				HUMFEN1.PRO
204	EFHLSRVLQELGLNQEVDLCIILGSDYCESIRGIGAKRAVDLIQK--	HKSIEEIVRRLDPS----	KY				MUSFEN1.PRO
204	EIDTELVLRGDLTIEQFVDLCIMLGCDYCESIRGVGPVTALKIKT--	HGSIEKIVEFIESGESNNTKW					YST510.PRO
198	FYDAESILKLLGLDRKNMIELAQLGSDYTNGLKGMPVSSIEVIAEF--	GNLKNFKDWYNNNGOFDKRK					YSTRAD2.PRO
198	LYLMDDMKREFNVNQMDLIKLAHLGSDYTMGLSRVGPVLAELIHEFPDGTGLFEFKKWFQRLSTGHAS						SPORAD13.PRO
198	YYQYVDFHNLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPFGHGLEPLLK	FSEWHEAQKNP					HUMXPG.PRO
119	YYQYVDFYSQLGLDRNKLINLAYLLGSDYTEGIPTVGCVTAMEILNEFPGRGLDPLLK	FSEWHEAQNNK					MUSXPG.PRO
198	YYQYADIHNLGLDRSKLINLAYLLGSDYTEGIPTVGYVSAMEILNEFPQGQGLEPLVK	FEKWSEAQKDK					XENXPG.PRO
175	-----	SSTACLHDIMHLSLGRMFM-----					CELRAD2.PRO

FIG. 70B

	290	300	310	320	330	340	350
251	LKKEVEYYDEIKRIFKEPKV-----	-----	-----	-----	-----	-----	-----
265	QKQSDVDLYAIKEFFLNPPV-----	-----	-----	-----	-----	-----	-----
269	PVPENWLHKEAHQLFLEPEV-----	-----	-----	-----	-----	-----	-----
267	PVPENWLHKEAQQLFLEPEV-----	-----	-----	-----	-----	-----	-----
272	KIPEDWPYKQARMFLDPEV-----	-----	-----	-----	-----	-----	-----
265	QETENKFEKDLRKKLVNNEIILDDDFPSVMVYDAYMRPEVDHDTTPFVWGVDPDMLRSFMKTQLGWPHE	-----	-----	-----	-----	-----	-----
268	KNDVNTPVKKRINKLVGK-IILPSEFPNPLVDEAYLHPAVDDSKQSFQWGIIPDLDELQRFLMATVGWSKQ	-----	-----	-----	-----	-----	-----
268	KIRPNPHDTKVKKKL--RTLQLTPGFNPAPAAEAYLKPVVDDSKGSFLWGKPDLDKIREFCQRYFGWNRT	-----	-----	-----	-----	-----	-----
268	KVAENPYDTKVKKKL--RKLQLTPGFNPAPADAYLRPVVDDSRGSFLWGKPDVDKIREFCORYFGWNRM	-----	-----	-----	-----	-----	-----
268	KMRPNPNDTKVKKKL--RLLDLQQSFNPAPASAYLKPVVDESKSAFSWGRPDLEQIREFCESRFGWYRL	-----	-----	-----	-----	-----	-----
194	-----EKKVSRPHLISAILLGCDYFORGVQNIIVSFD-ILGEFGDDGNEEIDPHVILDRFASYVRE	-----	-----	-----	-----	-----	-----
	290	300	310	320	330	340	350
300	RVKKHVVDKLYNLIA-----	-----	-----	-----	-----	-----	-----
314	RVKNGLERLKKAI-----	-----	-----	-----	-----	-----	-----
320	RIRSGVKRLSKSRQGS-TQGRLLDDFFKVT-----	-----	-----	-----	-----	-----	-----
318	RIRSGVKRLSKSRQGS-TQGRLLDDFFKVT-----	-----	-----	-----	-----	-----	-----
323	RVKSGISRLKKGLKSG-IQGRLLDGFFOVV-----	-----	-----	-----	-----	-----	-----
335	KSDEILIPLIIRDVNRKK-----	-----	-----	-----	-----	-----	-----
337	RTNEVLLPVIQDMHKKOF-----	-----	-----	-----	-----	-----	-----
336	KTDESLLFPVLKQLDAQQTQLRIDSFFRLAQKEKEDAKRIKSQRLNRAVTCMLRKEKEAAASEIEAVSVAM	-----	-----	-----	-----	-----	-----
336	KTDESLLPVLKHLNAHQTLRIDSFFRLAQKEKQDAKLKSHRLSRAVTCMLRKEEREKAPELTKVTEAM	-----	-----	-----	-----	-----	-----
336	KTDEVLLPVLKQLNAQQTQLRIDSFFRLAQKEAAG---LKSQRLRAVTCMLRKEERDVEAEVEAAVAM	-----	-----	-----	-----	-----	-----
257	EIPARSEDTRKRLRRKKYNFPVGFPCNDAVHNAITMYLRPPVSSEIPKIIPR-----	-----	-----	-----	-----	-----	-----
	360	370	380	390	400	410	420
300	RVKKHVVDKLYNLIA-----	-----	-----	-----	-----	-----	-----
314	RVKNGLERLKKAI-----	-----	-----	-----	-----	-----	-----
320	RIRSGVKRLSKSRQGS-TQGRLLDDFFKVT-----	-----	-----	-----	-----	-----	-----
318	RIRSGVKRLSKSRQGS-TQGRLLDDFFKVT-----	-----	-----	-----	-----	-----	-----
323	RVKSGISRLKKGLKSG-IQGRLLDGFFOVV-----	-----	-----	-----	-----	-----	-----
335	KSDEILIPLIIRDVNRKK-----	-----	-----	-----	-----	-----	-----
337	RTNEVLLPVIQDMHKKOF-----	-----	-----	-----	-----	-----	-----
336	KTDESLLFPVLKQLDAQQTQLRIDSFFRLAQKEKEDAKRIKSQRLNRAVTCMLRKEKEAAASEIEAVSVAM	-----	-----	-----	-----	-----	-----
336	KTDESLLPVLKHLNAHQTLRIDSFFRLAQKEKQDAKLKSHRLSRAVTCMLRKEEREKAPELTKVTEAM	-----	-----	-----	-----	-----	-----
336	KTDEVLLPVLKQLNAQQTQLRIDSFFRLAQKEAAG---LKSQRLRAVTCMLRKEERDVEAEVEAAVAM	-----	-----	-----	-----	-----	-----
257	EIPARSEDTRKRLRRKKYNFPVGFPCNDAVHNAITMYLRPPVSSEIPKIIPR-----	-----	-----	-----	-----	-----	-----

FIG. 70C

	430	440	450	460	470	480	490
314	-----	-----	-----	-----	-----	-----	MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	PFUFEN1.PRO
348	-----	-----	-----	-----	-----	-----GSL	HUMFEN1.PRO
346	-----	-----	-----	-----	-----	-----GSL	MUSFEN1.PRO
351	-----	-----	-----	-----	-----	-----PK-T	YST510.PRO
357	KRINEFF	-----	-----	-----	-----	-----	YSTRAD2.PRO
359	SNLTQFFEGGNTNVYAPRVAYHFKSKRL	ENALSSFKNQISNQSPMSE	EQADADAFGESKGSDELOSRIL				SPORAD13.PRO
406	EKEFELLDKAKRKTQKRGITNTLEESS	LKRRLSDSKRNTCGGFLGETCLSESSD	GSSSEHAESSLM				HUMXPG.PRO
406	EKEFELDDAKGKTOKREL	PK-----KETSVPKRRRPSGNGGFLGDPYCSESPQESSCEDGEGSSVM					MUSXPG.PRO
403	ERECTNQRKGGQKTNTKS	-----QGTKRKRKPTESQEDQDPGGGFIGIELKTLSSKAYSSD	-----				XENXPG.PRO
322	MKECGWPATRTQKELALSIRRKVHL	TTTVAQTRIPDFFAATKSKNFTPIVEPCE	SDLEYISANN-----T				CELRAD2.PRO

	500	510	520	530	540	550	560
314	-----	-----	-----	-----	-----	-----	NKTKQKTL MJAFEN1.PRO
327	-----	-----	-----	-----	-----	-----	KSGKQSTL PFUFEN1.PRO
352	SAKRKEPEPKGST	-----	-----	-----	-----	-----	KKKAKTGAAG HUMFEN1.PRO
350	SAKRKEPEPKGPA	-----	-----	-----	-----	-----	KKKAKTGGAG MUSFEN1.PRO
354	KEQLAAAKRAQE	-----	-----	-----	-----	-----	NKKLNKNKNK YST510.PRO
364	-----	-----	PREYISGDKKLNTSKRISTATGKL	-----	-----	-----	KK YSTRAD2.PRO
429	RRKKMMASKNSSDSDSEDN	FLASLTPKTNSSSISIENLPRKTKLSTSL	-----	-----	-----	-----	KKP SPORAD13.PRO
476	NVQRRTAAKEPKTSASDSONSVKEAPV	KNGGATSSSDSDDDGGKEKMLV	TARSVFGKKRRKLRRARG				HUMXPG.PRO
469	SARQSAAESKIGCSDV	PDVLRDSPHGRQGC	VSTSSDSEDGEDKAKTVLVTARPVFGKKRRKLKSMK				MUSXPG.PRO
458	-----GSSSDAEDLP	SGLIDKQSQSGIVGROKASNKV	ESSSSDDEDRVTMTAKPVFQGGKTKSKTMKE				XENXPG.PRO
387	WMRKRKRSESPQILQHHAKRQVPDRK	-----	-----	-----	-----	-----	RSVKIRAFKPYPTDVI CELRAD2.PRO

FIG. 70D

322 DAWFKZ
335 ESWFKR
375 KFKRGK
373 KFRRGK
377 VTKGRR
390 ---RKM
483 SKRRRK
546 RKRKTZ
538 RRKKKT
523 TVKRK
429 ELGDSD

MJAFEN1.PRO
PFUFEN1.PRO
HUMFEN1.PRO
MUSFEN1.PRO
YST510.PRO
YSTRAD2.PRO
SPORAD13.PRO
HUMXPG.PRO
MUSXPG.PRO
XENXPG.PRO
CELRAD2.PRO

FIG. 70E